

FIGURE 1

ID-65

Clone 3-60

5

GTGTTATGATGAAAAAAGGACAAGTAAATGATACTAAGCAA
 TCTTACTCTCTACGTAATATAAATTGGTTAGCATCAGTAA
 TTTAGGGTCATTCAATGGTCACAAGTCCTGTTTGCAGGA
 TCAAACATACATCGGTTCAAGTTAATAATCAGACAGGCACTAG
 10 TGTGGATGCTAATAATTCTTCCAATGAGACAAGTGCCTCAAGT
 GTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATAAAG
 TTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGAGAGACAAAGCCAATGGTGGAAAAAACATTACCTG
 15 AACAAGGGAATTATGTTATAGCAAAGAAACCGAGGTGAAAA
 ATACACCTCAAAATCAGCCCCAGTAGCTTCTATGCAAAGAA
 AGGTGATAAAGTTTCTATGACCAAGTATTAATAAAGATAAT
 GTGAAATGGATTTCATATAAGTCTTTGGTGGCGTACGTCGAT
 ACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAGAGA
 20 CTAAAGCACCTACTCCTGTAACAAATTCAAGGAAGCAATAATC
 AAGAGAAAATAGCAACGCAAGGAAATTATACATTTCACATA
 AAGTAGAAGTAAAAAATGAAGCTAAGGTAGCGAGTCCAACTC
 AATTACATTGGACAAAGGAGACAGAATTTCACGACCAAA
 TACTAACTATTGAAGGAAATCACTGGTTATCTTATAAATCATT
 25 CAATGGTGTGCGTGTGTTGCTAGGTAAAGCATCTTCA
 GTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCCGTATTACTAAAATGGTAGACTGACTATTCTAACG
 AAACAACATACAGGTTTGATATTAAATTACGAATATTAAAGA
 TGATAACGGTATCGCTGTTAAGGTACCGGTTGGACTGAA
 30 CAAGGAGGGCAAGATGATATTAAATGGTACAGCTGTAAC
 ACTGGGATGGCAACTACAAAGTAGCTGTATCATTGCTGAC
 CATAAGAATGAGAAGGGTCTTATAATATTCAATTACTACC
 AAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACCTAAAG
 TGACAGTAGCTGGAACTAATTCTCTCAAGAACCTATTGAAAAA
 35 TGGTTACCAAAAGACTGGTGTATAATATTACGGAAGTACT
 GAAGTAAAAAAATGAAGCTAAATATCAAGTCAGACCCAATT
 ACTTTAGAAAAAGGTGACAAATAATTATGATCAAGTATTG
 ACAGCAGATGGTACCAAGTGGATTCTACAAATCTTATAGTG
 GTGTCGCTGCTATATTCTGTAAAAAGCTAACTACAAGTAG
 40 TGAAAAAGCGAAAGATGAGGGACTAAACCGACTAGTTATCC
 CAACTTACCTAAAACAGGTACCTATACATTACTAAACTGTA
 GATGTGAAAAGTCACCTAAAGTATCAAGTCAGTCCAGTGGAAATT
 AATTTCAAAAGGGTAAAAAATACATTATGATCAAGTGTAA
 GTAGTAGATGGTCATCAGTGGATTCTACACAAGAGTTATTCCG
 GTATTGTCGCTATATTGAAATTAA

MFMMKKGQVNDTKQSYSRKYKFGLASVILGSFIMVTSPVFADQTSVQVNN
 5 QTGTSDANNSSNETSASSVITSNNDSVQASDKVVNSQNTATKDITPLVETK
 PMVEKTLPEQGNVYVSKETEVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDN
 VKWISYKSFGGVRRYAAIESLDPSPGGSETKAPTPVTNSGSNNQEKIATQGNYT
 FSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTIEGNQWLSYKSFNGVRRFV
 10 LLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTGFIDILITNIKDDNGIA
 AVKVPVWTEQGGQDDIKWYTAVTTGDGNYKVAVSFAHKNEKGLYNIHLY
 YQEASGTLVGVTKVTVAGTNSSQEPIENGLPKTGVYNIIGSTEVKNEAKISS
 QTQFTLEKGDKINYDQVLTADGYQWISYKSYGVRRYIPVKLTTSEKAKDE
 ATKPTSYPNLPLKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHYDQVLVVD
 GHQWISYKSYSGIRRYIEI*

15

Sequence description

A) Length: 1642 bp - 547 aa (full length gene)

B) Sequence Characteristics:

Potential leader peptide sequence

20

Orf is preceded by a potential Shine-Dalgarno sequence.

ID-66

25

Clone 3-5

ATGATATTGAGACGTCGAACTATTGTTTATGGCAACTGGGTATGCCATT
 30 TCTCTCATTCTTAGTATTCTAGCCTTAAATCTTATTCATAGTACTCCCTT
 GCAAACCAATGCAGCTTACGGAACCTTGCTCCTTCATTAAACCATTTTT
 GGGACAGATGGTTAGGTAGGGATATGTTGTCAGAACGATTAAGGACT
 TTATTCCTCTACAAGTCGGCTTATTAGGTGCCCTATGGGGTCATTCTG
 GCGACAGTTTGGAGTGCTTGCAGGTTAGGAAATAGCATTATTGATAAA
 35 ATAATAGCATGGTTAGTGATTGTTATTGGTATGCCTCATTGATTTTA
 TGATTCTCATTCTTTGTTGGAAAGGTGCTCAAGGGTCATCATTGC
 AACGGCTGTTACACATTGGCCTTCTTAGCAAGGCTTATCCGCAATGAAGT
 CTATCATCTAAAGAATAAGAATTGTCACACTTCTAAAAGTATGGGAAA
 AACGCCTTATTATATTGTGAGGCATCATTCCTGCCTTGATTGCTTCTCAA
 40 ATTTCTATTGGTTTATCCTCTATTCCACATGTCATCCTACATGAAGCAT
 CAATGACTTTCTAGGATTGGCTCTGCGGAACAAACCTCGGTTGGTA
 TCATTCTGTCAGAGGCAGCTAACGATATCTCTTGGAAATTGGTGGTTGG
 TTATCTTCCAGGACTTATCTTATTTGGTTGTCAATGCATTGATACTAT
 CGGAGAATCTTAAAGAAACTCTTACCCCTCAAACGTGATCATTAG

5 MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAALRNLAPSLNHLFGTD
 GLGRDMFVRTIKGLYFSLQVGLLGALMGVILATVFGVLAGLGNIIDKIIAWL
 VDLFIGMPHLIFMILISFVVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKNKE
 FVQLSKSMGKTPYYIVRHHILPLIASQIFIGFILLFPHVILHEASMTFLGFGLSAE
 QPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF
 *

10 Sequence description

A) Length: 822 bp - 274 aa (full length gene)
 B) Sequence Characteristics:
 Potential leader peptide sequence
 15 Orf is preceded by a potential Shine-Dalgarno sequence.

20 ID-78

25 Clone 3-5b

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTCACTCAA
 TACGGAAGATTTTAAAACCATTCAATCAACACCGATAAACGCGCTGA
 25 ATTTAGAAATTAAAAAGGTGAGTTATTAGCTATTATAGGTGCTAGTGGTT
 CGGGGAAGAGTTATTAGCACATGCTATTATGGATATTCTTCCTAAAAATG
 CATCTGTAACAGGAGATATGATTATCGTGGTCAATCACTAAATTCTAAAC
 GCATTAAACAGTTGCGAGGAAAAGATATTACGTTGATTCCACAATCAGTTA
 30 ATTATTAGATCCATCTATGAAAGTCAAACATCAGGTGCGCTAGGTATCT
 CAGAAAATTCAAAGGCTACTCAAGAAGGATTGTTCAACAGTTGGTTAA
 AAGAAAGTGATGGTACTGGATCCTTCCAACCTTCTGGCGGAATGCTCC
 GACGTGTTTGTACACGTGATTAGTGATAAGGTTCTTGATTATTGC
 GGATGAGCCCACCCCTGGATTACATCCAGATGCTCTGCAAATGGTTTACA
 35 CCAACTACGCTCCTTGCAGATAAAGGAATAAGCGTTATATTACTCA
 TGATATTGTAGCAGCTAGTCAAATTGCTGATCGTATTACTATTAAAGA
 GGGAAAAGCTATTGAAACAGCTCCAGCTAGTTCTTAGCGGAAATGGAG
 AGCAGTTACAAACAGAATTGCTAGAAGTTATGGCGCTCTCCCACAGC
 AAGAATTGGAAAGGAGTTACTCATGACCTTAGAGGCTAA

40 MTETLLSIKDSLITFTQYGRFLKPFQSTPIQALNLEIKKGELLAJIGASGSGKSLL
 AHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITLIPQSVNYLDPSMK
 VKHQVRLGISENSKATQEGLFQQFGLKESDGDLDPFQLSGGMLRRVLFTTCIS
 DVVSLIIADEPTPGLHPDALQMVLQDQLRSFADKGISVIFITHDIVAASQIADRITI
 FKEGKAIETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTHDLRG*

Sequence description

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A) Length: 804 bp - 268 aa (full length gene)

B) Sequence Characteristics:

No obvious leader peptide sequence

Orf is preceded by a potential Shine-Dalgarno sequence.

10

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified downstream and fully sequenced.

15

ID-79

Clone 3-5c

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GTCCATCTGGGGTGGTCCCGATTGGTATTCTTCTCCGATAGGTACTTGAGTCAAGATATTACGTTAGCTGATCGTATTAAGCACCTATTACCTGTTTACCGGTAAGTATTCTAGGCATTGCCAATGTAACTCTTCATACTAGAACTAAATGATGTCGGTACTTCTAGTGAATATGCTTATTGCCAGAGCGCGTGGGGAAACGGAATGGCAAATTAAATCATTGCTTAGAAATGCTATCGTACCAAGCTATTACACTGCATTTCCTATTGGAGAATTGTTGGAGGATCCGTTCTGCTGAGCAAGTTCTCATATCCAGGACTAGGGCTACCCTAACCTGAAGCAGGACTTAAAAGTGATACACCGCTACTTCTAGCTATTGTGATGATAGGGACATTATTGTTTGCAGGCAATCTTATTGCGGATATTAAATAGCATAATCAATCCACAGTTAAGGAGAAAAGTATGA

30

VHLGWFPIGIGSSPIGTLSQDITLADRIKHLILPVFTVSILGIANVTLHTRTKMMSV
LSSEYVLFARARGETEWQIFKNHCLRNAIVPAITLHF SYFGELFGGSVLAEQVF
SYPGLGSTLTEAGLKSDTPILLAIYMI GTLFVFA GNIJADILNSUINPQLRRKV*

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Sequence description

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A) Length: 495 bp - 165 aa (partial gene sequence)

B) Sequence Characteristics:

40

N-terminus has yet to be determined.

This gene was not isolated using the LEEP system. However in determining a full length gene sequence for ID-76, this gene was identified upstream.

ID-80

5

Clone 2-17

10 TTGCGGACAATTACGTTCAAACACAATGAAACCGCGATCGTCAAAAAGCGA
AGGTAGGGCGGTAACTGCTAAAAGATTATTACTGAAGATGGGAATTGA
CAAAGATTAGTCGTCGTTCGTTGGATGTTAGTGGTTATCTATTGTCTTAT
TATTGTCAGGATGTGTTTGGCCTCAAATTATGATTGAGGGGGTATCAAC
TCCGAATGTTCAGCGCTTCGGAAGAATTGTAGCTCTTTAGTACCAATTAA
TTCTTTCGTAGTTAGATCAGCTAACTAGCTTAAAGAGATTTTGGGTT
ATTGGTCAAAATGTAGTGAATATTTACTGCTGTTCTCTCATTATAGGGT
TAATCCCTAAAGCCAAGTTACGGAAATATAAAAGCGTTATATTACTTG
CTTTCTGATGTCTCTTTCATAGAGTGTACTCAAGTTAGATATT
AATAGATGCTAATCGGGTTTGAAATCGACGATCTATGGACAAATACCTT
AGGCGGTCTTCGCCATGGAGTTATCGAAACATAAAAGGTTGGCTTCT
AACTATTAGAAAATGA
20 MRTITFKHNETSSKSEGRAVMLKRLFTEDGELTKISRRFVWMLVVIYCLIIVR
MCFGPQIMIEGVSTPNVQRFRGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVV
NILLLFPLIIGLLSLKPSLRKYKSVILLAFLMSLFIECTQVVLIDIANRVFEIDD
LWTNTLGGPFALWSYRNIKGWLLTIRK*

Sequence description

30 A) Length: 579 bp - 193 aa (full length gene)
 B) Sequence Characteristics:
 Possesses a potential leader peptide sequence
 No obvious Shine-Dalgarno, but the 'TTG' codon
 may not be the actual translation start point.
35 A methionine (ATG) that occurs ~22 codons
 downstream of the 'TTG' is preceded by a
 potential Shine-Dalgarno sequence and may
 represent the actual start codon.

JD 81

40

Clone 3-1

TTGAAAAATTAAATCGTTATGTAGTTGGCGTTCTGGAGTCGTTTACATT
 TAATGCTAGGATCAACTTATGCTGGAGTGTGTTCGTAACCCAATTATCT
 CAGAGACTGGTTGGGATATTCATCAGTTCATCGCTTTAGTTGGCTAT
 TTTTGCTAGGAATGTCTGCAGCTTTATGGGACACTAGTAGAGCGTTT
 5 GGTCTAGGATAATGGGAATGATTCTGCTATTTATATGGAGCAGGGAAT
 GTGTTAACAGGCTTAGCCATTGAAACTCAGCAGTTAGGTTACTGTATGTT
 GCATACGGTATTTAGGAGGAATCGGACTTGGTCAGGTTATTAACCTCCA
 GTATCGACTATTAAATGGTTCTGATAGGAGGGACTAGCAACAGG
 10 ATTCGCTATTATGGGATTGGCTTGCTCTTAGTAACAAAGTCCGCTGCA
 CAATCCTTACTGATTAGGATTGGTGTGGGTAACAGTTTATTTGGGA
 TTAGTATTTTGTATGATGATTGCCTCACAAATTAAACAAACAC
 CTCAGGAAAAAAATAACTATTTGACTCACGATGGTAAAGAATGCTATG
 AATTCAAAATTATCACTGGATTAAGCAAACGTCGCTATAAAATCAA
 15 AACCTTTACATCATTGGTGACCTGTTATTAAATATTCGTGTGGCTTA
 GGTAAATATCAGCAGCTCACCAATGGCACAAGATTAGCAGGCTATTCC
 GCAGAACATCTGCAGCCTTATTAGTAGGGGTACTAGGGATATTAAACGGTTT
 GGACGCTCTGTTATGGCAAGTCTCTGACTACATTGGACGCCGTTGACC
 TTTATAATATTATTATTGTGAACTTATTATGACTTCTAGTTATTGGTC
 20 ATTCAATGCTATTGTATTGCAATAGCGATGCTATTAAATGACTTGTAT
 GGTGCAGGTTTCCTTACCTGCTTCTAAAGTGTATTTGGAAACAA
 AGGAATTAGCTACTTACATGGTTATAGTTAACAGCATGGCAATAGCAG
 GTCTGTTGGGCCCTATTGTTATCAAAGACATATTCAATGGGAAATCCT
 ATCAATTGACATTAATGGTTGGTTATTCTTATTCTGATTGTGTTA
 TCTCTATATTAAAGAAAATTAACAAACTAAAGTTGTGTAG
 25 LKNLNRYVVAVSGVVLHMLGSTYAWSVFRNPIISETGWDISSLFAFSLAIFC
 LGMSAAFMGHLVERFGPRIMGMISAILYGAGNVLTGLAIETQQLWLLYVAYG
 ILGGIGLGSYITPVSTIHKWFPDRRGLATGFAIMGFGFASLVTPLAQSLIRIG
 VGKTFYILGLVYFFVMMIASQFIKQPPQEKITILTHDGKKNAMNSQIITGLKAN
 30 VAIKSKTFYIIWLTFLNISCGLGLISAASPMQAQDLAGYSAESAALLVGVLGIFN
 GFGRLLWASLSDYIGRPLTFIILFIVNFIMTSSLFLSFNAIVFAIAMSILMTCYGA
 GFSLLPAYLSDIFGTKELATLHGYSLTAWAIAGLFGPLLSKTYSWGNSYQLTL
 MVFGFLFLGLLSLYLRKLTTKVV*

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Sequence description:

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A] Length 1221 bp - 407 a.a (full length gene).

B] TTG start codon with Shine-Dalgarno sequence upstream. Obvious signal peptide, with hydropathy plot exhibiting many possible membrane spanning regions, indicating protein to be transmembrane.

5 ID-82

Clone 48

10 ATGGCAGATAAAAACAGAACATTAACTTGTAGGTGCAGGATCTTCTAG
 CACACAAGAAAAATTGAAAAGCCTGCTCTTCGTTATGCAAGATGCGTG
 GCGTCGCTTGAAAAAAAACAAATTAGCAGTAGTTCACTCTATTATTAGC
 TCTTTACTTACTTTCTGTTAGCCTCAAATTATTTGTAACTCAGAAGGAT
 15 GCTAATGGGTTGATTGAAAGTAACGACATATCGCAACTACCACCT
 AAATTGAGTTCAAACCTCCTTTGGAATGGTAGCATTAAATCCAT**CA**
 MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRRLKKNKLAVVSLYLLA
 LLLTFSLASNLFVTQKDANGFDSKKVTTYRNLPKLLSNLPFWNGSINPS

20 Sequence description:

25 A] Current length is 303 bp - 101 aa
 B] No obvious signal peptide but Shine
 Dalgarno sequence upstream of the ATG start
 codon. Not identified directly using the LEEP system but was found
 directly downstream of ID-34 described in WO 00/06736.

30 ID-83

Clone 98

35 ATGAAAATAGTAGTACCACTAGTAATGCCTCGCAGTCTTGAAGAGGGCTCAAGA
 AATAGATTATCAAAATTGATAGTGTGATATTATTGAATGGCGAGCTGA
 TGCCTTACCAAAGGATGACATTATTAATGTAGCTCCAGCTATTTTGAGAA
 40 ATTCGCAGGTATGAAATTATTTACTTTCTGTTACAACGCGTGAAGGTGG
 TAATATTGTCTTATCTGATGCTGAGTATGTTGAGTTAATCCAGAAAATTAA
 TTCTATCTACAATCCAGATTATATTGATTTGAGTATTTCACATAAAGAA
 GTTTTCAAGAAATGCTAGAATTCAAATTAGTCCTGTCTTATCACAAATT
 TTCAAGAGACACCGGAGAATTATGGAGATATTTCAGAATTAACAGCC
 CTAGCACCACGAGTTGTGAAATCGCAGTAATGCCAAAGAATGAACAAAGA

5 TGTCTTAGACGTTATGAATTACACTCGCGGTTCAAGACTATTAATCCTGA
 TCAAGTTTATGCGACGGTATCTATGAGTAAAATTGGACGTATTCCTCGTTT
 GCTGGTGATGTAACTGGATCTAGTTGGACATTGCATATTAGATTCATCT
 ATCGCACCCGGACAAATTACTATTCAGAGATGAAGCGTGTCAAAGCATT
 GCTTGACGCTGACTGA

 10 MKIVVPVMPRSLEEAQEIDLSKFDSVDIIEWRADALPKDDIINVAPAIFEKFAG
 HEIIFTFRRTTREGGNIVLSDAEYVELIQKINSIYNPDYIDFEYFSHKEVFQEMLEF
 PNLVLSYHNFQETPENIMEIFSELTALAPRVVKIAVMPKNEQDVLDMNYTRG
 FKTINPDQVYATVSMSKIGRISRFAGDVTGSSWTFAYLDSSIAPGQITISEMKRV
 KALLDAD*

15 Sequence description:
 A] Length 678 bp, 225 aa (full length gene)
 B] No obvious signal peptide, but there is a
 Shine Dalgarno immediately upstream of ORF.

20 ID-84

25 Clone RS-52

30 ATGAAAGACTTATTGCAACAAACAGAACATCATCAAGGAAACAGGAACA
 AGATAGAATTGTCATTACATAAAACAACATGTTGAGTTAACAAATGGTA
 ATCAAATAAAAAAAATTGAGTTATCGACTTCAAAAAATGAGATGACA
 GGTACATGGGAATTCTACTAAAATTAAATGAACAAATTTCGATTAGTTT
 TCTGAAGATAGAATTGGTGGTAAACTAGAGCATTAGGATATCAACCGAA
 TGAAATAGGTTTCAAAGGACATCAATAGTAATAATCAAATGTTAATGA
 TATTGAAGTGATTATATGAAGAAAGAATAG

35 MKDLFATTEASSRKQEQRIVNYIKQHVELTNGNQIKKIEFIDFQKNEMTGTW
 GISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSKDINSNNQNVNDIEVIYMK
 KE*

40 Sequence description:
 A] length: 333 bp - 111 aa (partial sequence)
 B] No obvious Shine Dalgarno sequence upstream
 of the ATG start codon, and no obvious signal
 peptide within the protein.

ID-85

5

Clone RS-53

10 ATGAAAAAAACGTATATGGTATTGATAATAATAATCACAGTAATTAGGA
GGACTAGCCATGAAAAACTTATTGCAACAAACAGAAGCATCATCAAGGAA
ACAGGAACAAAGATAGAATTGTCAATTACATAAAACAAACATGTTGAGTTAA
CAAATGGTAATCAAATAAAAAAAATTGAGTTATCGACTTCAAAAAAAAT
15 GAGATGACAGGTACATGGGAATTCTACTAAAATTAAATGAACAATTTCG
ATTAGTTTCTGAAGATAGAATTGGTGGTAAACTAGAGCATTAGGATAT
CAACCGAATGAAATAGGTTTCAAAGGACATCAATAGTAATAATCA

20 MKKRIWYLIITVILGGLAMKNLFATTEASSRKQEQRIVNYIKQHVELTNGN
QIKKIEFIDFQKNEMTGTWGISTKINEQFSISFSEDRIGGKLRALGYQPNEIGFSK
DINSNNQ

Sequence description:

25 A] Length: 351 bp - 117 aa (Partial sequence)
B] Obvious signal peptide and Shine Dalgarno sequence upstream of the ATG start codon.

30
ID-86

Clone ID-74

35 ATGTCAAATCAATATGATTATATCGTTATTGGTGGAGGTAGT
GCAGGGCAGTGGTACCGCTAATAGGGCAGCCATGTATGGAGC
AAAAGTCCTGTTAATTGAAGGTGGACAAGTAGGTGGAACCTG
TGTAACTTAGGTTGTGTACCTAAGAAAAATCATGTGGTATGG
TGCACAAGTTCTGAGACACTCCATAAGTATAGTTCAGGTTA
TGGTTTGAAGCCAATAATCTTAGTTGATTTACTACTCTA
AAAGCTAACCGCGATGCTTACGTGCAGCGGTCTAGACAGTCG
TATGCCGCTAATTTGAGCGTAATGGGGTCGAAAAGATTGAT
GGATTGCTCGTTTATTGATAACCATACTATTGAAGTGAATG
GTCAGCAATATAAGCTCCTCACATTACTATTGCAACAGGTG

GACACCCTTTACCTGATATTATTGGAAGTGAACCTGGTG
 AGACTTCTGATGATTTTTGGATGGGAGACCTTACCAAATT
 TATATTGATTGGGGCGGGCTATATCGCGGCAGAACCTGC
 TGGAGTGGTAATGAATTAGGCCTGAAACCCATCTTCATT
 5 TAGAAAAGACCATATTCTACCGGGATTGATGACATGGTAAC
 AAGTGAGGTTATGGCTGAAATGGAGAAATCAGGTATCTCTT
 ACATGCTAACCATGTACCTAAATCTCTAAACCGCGATGAAGG
 TGGCAAGTTGATTTGAAGCTGAAAATGGGAAAACGCTTGT
 CGTTGATCGTGTAAATAGGGCTATCGGCCGTGGACCAAATGT
 10 AGACATGGGACTTGAAAATACCGATATTGTTAAATGATAA
 AGATTATATCAAAACAGATGAATTGAGAATACCTCTGTAGA
 TGGCGTGTATGCTATTGGAGATGTTAATGGGAAAATTGCCTT
 GACACCGGTAGCAATTGCAGCAGGTCGCTTATCAGAAAG
 ACTTTTAATCATAAAGATAACGAAAATTAGATTACCATAA
 15 TGTACCTTCAGTTATTTTACTCACCCCTGTAAATTGGGACGGTA
 GGACTTTCAGAAGCAGCAGCTATCGAGCAATTGGGAAAAGAT
 AATATCAAAGTCTATACATCAACTTTACCTCTATGTATACGG
 CTGTTACCACTAGTAATGCCAAGCAGTTAAGATGAAGCTCATAA
 CCCTAGGAAAAGAGGAAAAGTTATTGGGCTTCATGGTGTG
 20 GTTATGGTATTGATGAAATGATTCAAGGTTTCAGTGCTAT
 CAAAATGGGGCTACTAAAGCAGACTTGTGATGATACTGTTGC
 TATTCACTGGACTGAGGAATTGTTACAATGCGCTA
 A
 25 MSNQYDYIVIGGGSAGSGTANRAAMYGAKVLLIEGGQVGGTC
 VNLGCVPKKIMWYGAQVSETLHKYSSGYGFEANNLSFDFTTLK
 ANRDAYVQRSRQSYAANFERNGVEKIDGFARFIDNHTIEVNGQ
 QYKAPHITIATGGHPLYPDIIGSELGETSDDFFGWETLPNSILIVG
 AGYIAAEALAGVNELGVETHLAFRKDHILRGFDDMVTSEVMAE
 30 MEKSGISLHANHVPKSLKRDEGGKLIFEAENGKTLVVDRVIWAI
 GRGPNVDMGLENTDIVLNDKDYIKTDEFENTSDGVYAIQDVN
 GKIALTPVIAAGRRLSERLFNHDNEKLDYHNPSVIFTHPVIG
 TVGLSEAAAIEQFGKDNIKVYTSTFTSMYTAVTSNRQAVKMKLI
 TLGKEEKVIGLHGVGYGIDEMIQGFSVAIKMGATKADFDDTVAI
 35 HPTGSEEFVTMR*

Clone RS-55

5 ATGACAAAAAAACATCTAAAACGCTGCCTGGCACTTACTACAGTATCA
 GTAGTGACATACAGCCAGGAGGTATATGGATTAGAAAGAGAGGAATCGGT
 CAAACAAGAACAAACCCAGTCAGCTCAGAAGATGATTGGTCGAAGAAG
 ATAATGAGAGGAAAACAAATGTTCTAAAGAGAATTCTACTGTTGATGAA
 ACAGTTAGTGTATTATTTCTGATGGAAATAGTAATAACTCTAGTTCTAAA
 10 ACCGAGTCAGTGGTAAGTGACCCCTAAACAAGTCCCCAAAGCAAAACCAGA
 GGTTACACAAGAAGCAAGCAATTCTAGTAATGATGCTAGCAAAGTAGAAG
 TACCAAAACAGGATACAGCTCAAAAAGGAAACTCTAGAAACATCAACT
 TGGGAGGCAAAAGATTCTGTAACTAGAGGGGACTTTAGTAGGTTTTCA
 AAATCTGGAATTAAAGTTATCTCAACATCACACTTGGTTTACCAAGT
 15 CATGCAGCAGATGGAACTCAATTGACACAAAGTAGCTAGCTTGCTTTACT
 CCAGATAAAAAGACGGCCATTGCAGAATATAACAGTAGGCTAGGAGAAA
 ATGGGAAACCGAGTCGTTAGATATTGATCAGAAGGAAATTATTGATGAG
 GGAGAAATTTAATGCTTACCAAGTTGACTAAGCTTACTATTCAAATGGT
 TATAAGTCTATTGGTCAAGATGCTTTGTGGACAATAAGAATATTGCTGAG
 GTTAACCTCCTGAGAGTCTCGAGACTATTCAGACTATGCTTTGCTCACA
 20 TGTCTTAAAACAAGTAAAGTTACCAAGATAACCTAAAGGTATTGGAGAA
 TTAGCTTTTTGATAATCAGATTGGTGGTAAGCTTACTGCCACGTCACT
 TGATAAAATTAGCAGAACCGCGCTTCAAATCTAATCGTATTCAAACAGTTG
 AATTGGGAAGTAAGCTTAAGGTTATAGGAGAACAGTTCAAGAT
 25 AATAATCTGAGGAATGTTATGCTTCCGGATGGACTTGAAAAAATAGAAC
 AGAAGCTTTACAGGAATCCAGGAGATGAACATTACAACAAATCAGGTTG
 TATTGCGCACAAGGACAGGCCAAATCCACATCAACTGCGACTGAGAAC
 ACTTACGTCAATCCGGACAAATCATTGTGGCGTGCACACACCTGATATGGAT
 TATACCAAATGGTTAGAGGAAGATTTACCTATCAAAGGTTAGTGTACAG
 30 GTTTTCAAATAAAGGCTTACAAAGGTAAGACGTAATAAAACTAGA
 AATTCCAAAACAACACAATGGTATTACTATTGAAATTGGTATAACGC
 TTTCGCAATGTTGATTTCAAAGTAAAACCTACGTAATATGATTGGA
 AGAAATAAAGCTCCCTCAACTATTGGAAAATAGGTGCTTTGCTTTCA
 ATCTAATAACTGAAATCCTTGAAGCAAGTGAAGATTAGAACAGGTTA
 35 AAGAGGGAGCCTTATGAATAATCGTATTGGAACCTAGACTGAAAGAC
 AAACTTATCAAATAGGTGATGCTGCTTCCATATTAATCATATTATGCC
 ATTGTTCTCCAGAATCTGTACAAGAAATAGGACGTTCAGCTTCGACAA
 ATGGTGCCTTCACCTTATGTTATGGAAAATAAGGTTAAACAAATTGGT
 GAAATGGCTTTTATCCAATAAAACTGGAAAGTGTAAATCTCTGAGCAA
 40 AAACAATTAAAGACAATTGAGGTCCAAGCTTTCGGATAATGCCCTAGT
 GAAGTAGTCTTACCGCCAATTACAGACTATTGCTGAAGAGGGCTTC
 AGGAATCATTGAAAGAAGTGAAGGGTTCATCTACATTATCTCAGATTACT
 TTAATGCTTTGATCAAATGATGGGGACAAACGCTTGGTAAGAAAGTG
 GTTGTAGGACACATAATAATTCTCATATGTTAGCAGATGGTGAGCGTTT
 ATCATTGATCCAGATAAGCTATCTTCTACAATGGTAGACCTGAAAAGGTT

TTAAAAATAATCGAAGGTTAGATTACTCTACATTACGTCAGACTACTCAA
 ACTCAGTTAGAGAGAAATGACTACTGCAGGTAAAGCGTTGTTATCAAAATCT
 AACCTCCGACAAGGAGAAAAACAAAAATTCCCTCAAGAAGCACAATT
 CCTGGTCGCGTTGATTGGATAAAGCCATAGCTAAAGCTGAGAAGGCTT
 5 AGTGACCAAGAAGGCAACAAAGAATGGCATTGCTTGAGAGGAGTATTA
 ACAAAGCGGTATTAGCTTATAATAATAGTGTATTAAAAAGCTAATGTTA
 AGCGCTGGAAAAAGAGTTAGACTTGCTGACAGATTAGTCGAGGGAAAA
 GGACCATTAGCGCAAGCTACAATGGTACAAGGAGTTATTATTAAAGAC
 GCCTTACCATGCCAGAATATTATATCGGATTGAACGTTATTTGACAA
 10 GTCTGGAAAATTGATTATGCACCTGATATGAGTGATACTATTGGCGAGGG
 ACAAAAGATGCATATGGTAATCCTATATTAAATGTTGACGAGGATAATG
 AAGGTTATCATACTTGGCAGTTGCCACTTAGCTGATTATGAAGGTCTT
 ATATTAAAGATATTAAATAGTCCCTGATAAGATAAAGCAATACGCC
 15 AGATTCCCTGGCAAATATCATAGATTAGGAATTCCAAGCTATCCGAA
 ATGCAGCGGCAGAAGCAGACCGATTGCTCCTAACAGACACCTAACGGGTAC
 CTAATGAAGTCCCAATTATCGTAAAAACAAATGGAGAAAAATTAAA
 ACCAGTTGATTATAAACGCCGATTTAATAAGGCTTACCTAATGAAAAA
 GGTAGACGGTGATAGAGCGGCTAAAGGTCTAACATATAATGCGGAGACTA
 20 ATAATTCTGTAGCTGTAACACCAATAAGGTCCGAGCAGCAATTACATAAGT
 CACAGTCTGATGTAACACCAAAAGTCTAAAAATAATTATAT
 ACGAGATTCTAGGATACGTTAGTTATGTTGCTTCTAGTAACGCTGG
 GAAAAAAAGGAAAACGAGCAAGAAAATAA

25 MTKKHLKTLALALTTSVVTYSQEYGLEREESVKQEQTQSASEDDWFEEDN
 ERKTNVSKENSTVDETVSDLFSDGNSNNSSKTESVVSDFPKQVPKAKPEVTQE
 ASNSSNDASKVEVPKQDTASKKETLETSTWEAKDFVTRGDTLVGFSKGINKL
 SQTSHLVLPSHAADGTQLTQVASFAFTPDKKTAIAEYTSRLGENGKPSRLDIDQ
 KEIIDEGEIFNAYQLTKLIPNGYKSIGQDAFVDNKNIAEVNLPESLETISDYAF
 AHMSLKQVKLPDNLKViGELAFFDNQIGGKLYLPRHLIKLAERA
 30 FKSNSRIQTV
 EFLGSKLKViGEASFQDNNLRNVMLPDGLEKIESEAFTGNPGDEHYNNQVVL
 TRTGQNPHQLA
 35 TENTYVNPDKSLWRATPDMDYTKWLEEDFTYQKNSVTGFS
 NKGLQKVRRNKNLEIPKQHNGITITEIGDNAFRNVDFQS
 KTLRKYDLEEIKLPS
 TIRKIGAFAFQSNNLKS
 FEASEDLEEIKE
 GAFMNNRIGT
 LLDLKD
 KLIKIGDAAFH
 INHIYAI
 VLPESVQE
 IGRSAFRQNGAL
 HLMFIGNK
 VKTIGEMA
 FLSNK
 LESVNL
 SEQKQLK
 TIEVQAF
 SDNAL
 SEVVL
 PPNL
 QTI
 REEAF
 KRNL
 KEV
 KGS
 STLS
 QITF
 NAFDQNDGDK
 KRGK
 VV
 VRTHNN
 SHML
 ADGER
 FI
 IDP
 DKL
 SS
 TMD
 LEK
 KVL
 KII
 EGLD
 YSTL
 RQTT
 QT
 FRE
 MTT
 AG
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 ALL
 SKS
 NLR
 QGE
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 QFL
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 LGR
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 *

Sequence description:

5 A] Length 3168 bp - 1056 aa (Partial sequence)
 B] Obvious signal peptide with Shine Dalgarno
 sequence upstream of the ATG start codon.

10 ID-88

Clone RS-56

15 GCAGGATACATCATGCACAAGCACGAGGCTATCGTGTATGCTGGGGTCA
 ACCCAGGAAGACATGTCGGCACAAGCTGAAGATTCTTACAGTCTGTACA
 CAATAAAGAGACGGGTAAGAGCGCTTTAATGACAAAGAACGACTAGCAA
 20 TT
 AGYIMHKHEAIVSCWGQPRKTCRHLKISLQSVHNKETGKSAFNDKERLAI

25 Sequence description:

30 A] Length:153 bp - 51 aa (partial sequence)
 B] No signal peptide visible, insufficient
 sequence data to determine the presence of a
 Shine Dalgarno sequence.

35 ID-89

Clone RS-58

40 GTGTCATTTATGCAAAGAAAATCCTATTAATCCATGAGTGTCTTACT
 TTAACAGCTTGTCTTATATCAGGATATGTGGTTAAAGATATTGCTATGTTA
 CATGCAGTATCTGCCAGTGAGAAGAAAGCAAATAATGTCAGTCCGAGAGA
 AAATCTCTACAGGGCTGTCAATGATAATTGGCTAGCCAATACAAAACCTCA
 AACAAAGGGCAGACTAGTGTAAATAGTTTCAGAAATTGAGGATAAATTAA
 AAGCAACTGTTAGTGTCTGATATGGCTAAAATGGCCTCAGGAAAGATTGA

5 AACAAACCAATGATGAACAGAAAAAAATGGTGCATACTATAAACAAAGGTA
 TGGACTTTAAAACAAGAGATAAAAATGGTCTCAAACCTCTAAAACCAGTT
 TTACAAAAACTGAAGCAGTCTCTTCAATGAAAGACTTCAAAGTTGGCC
 CATGATTGTGATGAGTGGTTGTTTACCATTTGGTTGACTGTGGAAA
 10 CCAATGCTCGAGATAATAGCCAAAAGCAATTGGTCTCGTCAAGCACCC
 GCATTACTTGAATCACCTGACCAATATAAGAAGGGCAATAAAGAAGGTGA
 GGCTAAATTATCAGCTTACCGTACTTCAGCAATGGCTTGCTAAACAAGC
 TGGAAAAAGTAACATTGAAGATAGAAAAGTAAACAAAGCTATAGCAT
 TTGATAGACTCTTATCAGAAAAAAACGCAAGTTGATCAAAGTAAAATCACA
 15 GCTGAAAGTGAGACAGCTGCGGGGCGATATAACCCTGAAAGTATGGAAAC
 GGTCACAATTACGCCAAGGAATTGACTTTAAAGAATTGATTGAAAGAAACT
 AGTTGGGCCAACGAATAAGGCAGTCAATGTAGAAGATAAAACTTATTITA
 AACAGGTTAATGATGTTATAAATAGTAAACAATTAGCCAATATGAAAGCA
 TGGATGATGATTCTATGCTAGTTGATCAATCAGATTCTAGGAGAACAA
 20 AATCGTCAAGCAGCGAGTGCTTTAAGAATGTTGCGTCTGGTTGACTCAG
 ATTGAATCGAAAGAAAAATGCTTACACCCAATTAG

25 MSFMQRKSYLKSMsvLTACLiSgyvvKDIAMLHAVSASEKKANNVSPREN
 LYRAVNDNWLANKLKQGQTSVNSFSEIEDKLKQLVSDMAKMASGKIETTN
 DEQKKMVAYYKQGMDFKTRDKNGLKPLKPVLQKLEAVSSMKDFQSLAHDF
 VMSGFVLPFGLTVETNARDNSQKQLVLRQAPALLESPDQYKKGNKEGEAKLS
 AYRTSAMALLQAGKSNIEDRKLVKQAIADFLLSEKTQVDQSKITAESETAA
 30 GRYNPESMETVHNYAKEDFKELIEKLVGPTNKAVNVEDKTYFKQVNDVINS
 KQLANMKAWMMISMLVDQSDFLGEQNRQAASAFKNVASGLTQIESKEMLT
 PN*

35 Sequence description:

A] Length: 1095 bp - 365 aa (full length gene)
 B] an GTG (possible ATG start codon located 7 bp
 further downstream) start codon with an obvious
 signal peptide. Shine Dalgarno sequence present
 upstream of the ORF.

40 ID-90

Clone RS-59

ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAGAAATTAAAATGAG
 TATTGATAAACTTAGATATAAAGAACCAAGAGAGTGAACATGACAAGCGAC
 CTACTTTTATTGGTAGTACTTAACTGTTACTGTAGCAGTTATATTGTC
 GTTATTTAAATATTTTTATAG

5

MEMPKRNELLNKEIKMSIDKRYKEPESEHDKRPTFYLVVLILVTAVILSLFK
 YFL*

10 Sequence description:

15 A] Length: 174 bp - 58 aa(full length gene)
 B] No obvious signal peptide, but Shine
 Dalgarno sequence is present upstream of ATG
 start codon.

20 ID-91

Clone RS-62 (partial sequence)

25

ATGCAGGTATTTAAATATTGTCATAAAATTCTTGATCCAGTTATTCTATA
 TGGGTTCGGGAGTTGTATGCTAATTGTCATGACAGGTTAGCCATGATAT
 TTGGAGTGAAGTTTCTAAAGCACTTGAAGGTGGTAT

30

MQVFLNIVNKFFDPVIHMGSVVMLIVMTGLAMIFGVKFSKALEGG

Sequence description:

35

A] Length:141 bp - 41 aa (partial sequence)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon with a possible signal peptide
 present

40

ID-92

Clone RS-69 (partial sequence)

5 ATGAAAAAGAAAACATCAGTGCTTATAACTTTAACGGCTCTTATCCTT
 TGTCTTTGACAGTGCTTTATCTTCCATTTATTGGATTATGACAGGAG
 CTTTAA

MKKKTFSAYNFLTALILCLLTVLFIFPFYWIMTGAF

10

Sequence description:

15

- A] Length: 110 bp -36 aa (Partial sequence)
- B] Possible signal peptide with Shine Dalgarno sequence directly upstream of the ATG start codon.

20

ID-93

25

Clone RS-70

30

ATGACTGAGAACTGGTTACATACTAAAGATGGTCAGATATTATTATCGT
 GTCGTTGGTCAAGGTCAACCGATTGTTTTTACATGGCAATAGCTTAAGT
 AGTCGCTATTTGATAAGCAAATAGCATATTTCTAAGTATTACCAAGTT
 ATTGTTATGGATAGTAGAGGGCATGGCAAAAGTCATGCAAAGCTAAATAC
 CATTAGTTCAAGGCAAATAGCAGTTGACTAAAGGATATCTTAGTCATT
 AGAGATTGATAAAAGTTATTGGTAGGCCATAGCGATGGTGCTAATTAGC
 TTTAGTTTCAAACGATGTTCCAGATATGGTAGAGGGCTTGCTTAAT
 TCAGGGAACCTGACTATTCACTGGTCAGCGATGGTGGGATATTCTTAGTA
 35 AGGATTGCCTATAAATTCTTCACTATTAGGGAAACTCTTCCGTATATG
 AGGCAAAAAGCTCAAGTTATTGCTTATGTTGGAGGATTGAAGATTAGT
 CCAGCTGATTACAGCATGTGCAACTCCTGTAATGGTTGGTGGAAAT
 AAGGACATAATTAAAGTTAAATCATTCTAAGAAACTTGCTTCTTATTCCA
 40 AGGGGGGAGTTTATTCTTACTGGCTTGGCATCACATTATTAAGCAA
 GATTCCCATGTTTAATATTGCAAAAAAGTTATCAACGATACTG
 AAAGGAGAAATTGTTGAAAAAGCTAATTGA

MTENWLHTKDGSIDIYRVVGQGQPIVFLHGNSLSSRYFDKQIAYFSKYYQVIV
 MDSRGHGKSHAKLNTISFRQIAVDLKDILVHLEIDKVLVGHSDGANLALVFQ

TMFPDMVRGLLLNSGNLTIHGQRWWDILLVRIA YKFLHYLGKLFPMRQKA
 QVISLMLEDLKISPADLQHVSTPVMVLVGNKDIKLNHSKKLASYFPRGEFYSL
 VGFHHIIKQDSHVFNIIAKKFINDTLKGEIVEKAN*

5

Sequence description:

10 A] Length: 744 bp - 248 aa (full length gene)
 B] No obvious signal peptide, but Shine
 Dalgarno sequence upstream of the ATG start
 codon.

15

ID-94

Clone RS-71

20

ATGGTAGCAAAAGAGTTAGGTAAAAATAGCTTACTATCCCAACTATTTGT
 TCTAATTGCTCCGCAGGTACTGCCATTGCAGTTGTATATAATGATGACCAT
 25 TCTTTCTTAAGATAACGGCTATCCCGAGTCTCCACTTCATATTTTATCAATA
 CACGGATCATTGCACAGGCACCAAGCAAATATTTTGGGCTGGTATTGGGG
 ACGGTATTCAAAAGCCCCTGAAGTAGAACGTGCTACCTTAGAGGCTAAG
 ACCAATAAAACTACCACATACTGCAGTGTAGGACAAGCAGTCGCTCTGTCT
 TCAAAGGAAGCTTTTATCAATTGGTGAACAAGGTCTAAAGACGTTGAA
 30 GCTAATTAGCTTCGCGTGCAGTTGAAGAAATTGCGCTTGATATCTTA
 MVAKELGKNSFTIPTICNSCAGTAIAVVYNDDHSFLRYGYPESPLHIFINTRIIA
 QAPSKYFWAGIGDGISKAPEVERATLEAKTNKLPTAVLGQAVLSSKEAFY
 QFGEQQLKDVEANLASRAVEEIALDIL

35

Sequence description:

40 A] Length: 405 bp - 135 aa (Partial sequence)
 B] No obvious Shine Dalgarno sequence upstream
 of the ATG start codon, probable signal
 peptide present at the N-terminus.

ID-95

Clone RS-73

5 TTGAGGGAAACTTACTGGAAAATTCAAGCGATTGCGATAAAATAATCTT
 GCAGAGTTTCTAGAGAAAGGAGGTAGATTATTGGAGTGGCAAGATCT
 AGCGCAGTTACCTGTATCTATTTAAAGACTATGTTACAGATGCTCAAGA
 CGCGGAAAAACCTTTATATGGACAGAAGTATTTTAAGGGAGATTAATCG
 CTCAAATCAAGAAATTATTTGCATATTGGCCGATGACTAAGACAGTCAT
 10 TCTGGGGATGTTAGATCGAGAATTACCACTTACAATTAGAATTAGCTAAAAAAG
 AAATCATCAGTCGTGGTTATGAACCAAGTTGTCGGAATTTGGAGGTCTCG
 CAGTTGTAGCTGATGAAGGAATTAAATTTCATTGGTTATTCCAGATGTT
 TTTGAGAGAAAATTGTCTATCTCAGATGGGTATCTTATAATGGTCGATTT
 15 ATTAGAAAGTATTTCCGGATTTATCAACCTATTGAGCACTTGAAGTA
 GAGACCTCCTATTGTCCTGGTAAGTTGATCTTAGTATAAATGGCAAAAAAA
 TTTGCTGGCTTGGCTAGCGCCGTATAAAGAATGGTATTGCGGTATCAATT
 TACCTTAGCGTTGTGGCGATCAAAAAGGGCGGAGTCAAATGATTCAGAT
 TTTTATAAGATTGGCTAGGTGATACGGGTAGTCCAATTGCTTATCCAAAT
 GTAGATCCTGAAATTATGGCTAATCTATCTGATCTATTAGATTGTCCTATG
 20 ACAGTAGAAGATGTTATTGATCGTATGTTGATTAGCCTAAACAAGTAGGT
 TTTAATGATCGTTACTGATGATTAGACCCGATTAGTTGCAGAGTTGAT
 AGATTTCAGGCTAAGTCTATGGCTAATAAGGGATGGTGAGCAGAGATGA
 ATAA

25 MRETYWKISSDCDKINLAEFSRERRSDLLEWQDLAQLPVSIFKDYVTDAQDAE
 KPFIWTEVFLREINRSNQEILHIWPMTKTVILGMLDRELPHLELAKKEIISRGYE
 PVVRNFGLAVVADEGILNFSLVIPDVFERKLSISDGYLMVDFIRSIIFDFYQPI
 EHFEVETSYCPGKFDLSINGKKFAGLAQRRIKNGIAVSIYLSVCGDQKGRSQMI
 30 SDFYKIGLGDGTGSPAYPNVDPEIMANLSDLLCPMTVEDVIDRMLISLKQVGF
 NDRLLMIRPDLVAEFDRFQAKSMANKGMVRDE*

Sequence description:

35 A] Length: 921 bp -307 aa (Full-length gene sequence)
 B] No obvious Shine Dalgarno sequence upstream
 of the TTG start codon or signal peptide
 visible. Actual start point may be a further
 40 85 bp downstream (TTG). This start point is
 preceded by a typical Shine-Dalgarno sequence.

ID-96

Clone RS-74

5

TTGGAAGGTTACTTATTGCATTGATTCCCAGTTGCGTGGGAAAGTATT
 GGATTGTTAGTAATAAAATTGGAGGGCGTCCAAATCAACAAACATTGG
 AATGACTTCTAGGACCATTGCTATTGCGATTATCGTATGGTTATTAAACA
 10 GCCAGAGATGACTGCCTCATGTGGATTTGGTATCTTAGGTGGTATCCT
 ATGGTCAGTCGGCCAAATGGTCAATTCAAGCAATGAAATATATGGGAG
 TCTCTGTTGCTAATCCACTGTCAAGTGGTGACAATTAGTAGGTGGAAAGCC
 TAGTTGGTGCTTAGTCTTCATGAATGGACTAAGCCAATCCAATTATT
 15 AGGATTGACAGCGTTGACATTATTAGTTATCGGCTCTATTCTCAAGTAA
 ACGTGATGTTCAGAACAGCTTGGCAACACATCAAGAGTTTCAAAAG
 GATTGCTACAATTGCTTATTCAACTGTAGGTTACATCTCGTACGCAGTTT
 ATTTAACACATTATGAAGTTCGACGCTATGGCCGTCTATTACCCATGGC
 TGTTGGAATGTGTCTAGGTGCAATTGTTCATGAAGTTCTGTGTTAACTTT
 20 GAGGCTGTTGTTAAAAATGATTACAGGTCTCATGTGGGCGTTGGT
 AATGTCTTCATGTTATTGGCAGCAGCTAACAGCAGGGCTAGCAATTGCTTT
 AGTTTTCTCACTGGAGTAATTATCTCTATTATTGGTGGTATTATT
 AGGTGAGACAAAAACGAAGAAAGAGCAGAAATGGGTTGTCATGGGTATC
 CTTTGTGTTATGGGTCTATATTACTGGTATTGTTAAATCTTATTAA
 25 MEGLLIALIPMFAWESIGFVSNKIGGRPNQQTFGMTLGALLFAIIVWLFKQPEM
 TASLWIFGILGGILWSVGQNGQFQAMKYMGVSVANPLSSGAQLVGGSLVGAL
 VFHEWTKPIQFILGLTALTLVIGFYFSKRDVSEQALATHQEFSKGFA
 30 TGYISYAVLFNNIMKFDAMAVILPMAVGMC
 LGAI
 C
 FMKFRVNFEAVVVKNMI
 TG
 L
 MWGVGVNVFM
 LAA
 KAGLAIAFSFSQLGV
 I
 SI
 IGGILFLGET
 K
 KEQK
 WVVMGILCFVMGAILLGIVKSY*

Sequence description:

35

- A] Length: 867 bp - 289 aa (full-length gene)
- B] Possible Shine Dalgarno sequence upstream of
GTG start codon, no obvious signal peptide
present.

40

ID-97

Clone RS-75

5 ATGACAACTTACTACGAAGCTATAAACTGGAACGAAATTGAAGATGTTAT
 TGATAAATCAACTTGGGAAAAACTAACCGAACAAATTGGCTCGATACAC
 GTATCCCTTATCAAATGACTTAGACGATTGGCGCAAACCTTCCGCTCAAG
 AAAAAGATCTTGGCAAGGTTGGAGGCTTAACCCACTTGATACCA
 10 TGCAATCAGAAACTGGTGTGAAGCTATTGCGCCGATGTCGCACGCCTC
 ACGAAGAAGCTGTCTAAACAATATTCAATTGGAATCTGTTACGCTA
 AATCTTATTCTCAATTTCCTCAACTTTAAATACTAAATCAGAAATTGAAG
 AAATTTGAGTGGACTAATAATAATGAGTTCTTCAAGAAAAAGCACGT
 ATTATCAATGACATTATGCTAATGGAAATGCCCTCAAAAAAAAGGTGGCT
 TCCACCTACCTCGAAACTTCCCTTTTATTCTGGCTTTCACACCTCTTA
 CTATTGGGAAATAATAAGTTAGCAAATGTTGCTGAAATCATTAAATTAAT
 15 TATTGCGTATGAAATCTGTACATGGTACTTATATCGGTTACAAATTCCAGCTT
 GGTTTAACGAATTACCAAGAGATGAGCAAGAGAATTTGCGTATTGGAT
 GTATGACCTCCTTATCAGCTGTATGAAAACGAAGAAAAATACACCAAGA
 CACTTATGATGGCGTAGGATGGACTGAAGAAGTTATGACCTTTACGCT
 ACAATGCTAATAAAAGCTTTATGAATTAGGACAAGATCCTTATTCCCAG
 20 ATACAGCAAATGATGTCACCCAATTGTTATGAATGGTATTCAACAGGAA
 CATCAAACCATGACTCTCTCAAGTAGGAAATGGTACCTACTGGTA
 GCGTTGAAGCTATGCATGATGACTATAACTATGGATTATAA

 MTTYYEAINWNEIEDVIDKSTWEKLTEQFWLDTRIPLSNDLDDWRKLSAQEK
 25 DLVGKVFGLTLLDTMQSETGVEAIRADVRTPHEEAVLNNIQFMESVHAKSY
 SSIFSTLNTKSEIEEIFEWTNNEFLQEKARIINDIYANGNALQKKVASTYLETF
 LFYSGFFTPLYLGNNNKLANVAEIIKLIIRDESVHGTYIGYKFQLGFNELPEDEQ
 ENFRDWMYDLYQLYENEKYTKTLYDGVGWTEEVMTFLRYNANKALMNL
 GQDPLFPDTANDVNPIVMNGISTGTSNHDFSQVGNGYLLGSVEAMHDDYN
 30 YGL*

Sequence description:

35 A] Length: 960 bp - 320 aa (full length gene)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon, but no signal peptide
 present.

40

ID-98

Clone RS-77 (partial sequence)

5 ATGAATTGGTCACGTACTGGGAACTCGTAAGAAATTAAATATCCTTATTCA
 AACCCCTCAGACTCTATCGGCACTAAGAAAAAGCAAGAAAAGCATCCTAA
 AAAAGAATTTCAGCTTATAAATCCATGTTAGAAATCAGTTATTTCAGAT
 TTTGCTCTTTCAATAATTATGTATTCTCTTGTATCACTGATTTAAAG
 10 AATATCCGGGCTATTCACGTTCTACATTGGTATCTTACACTAGTATCCAT
 TATCTACTCTTTATTGCGATGTACAGTGTCTATGAGAGTGACGATGTT
 AA

MNWSRIWELVKINILYSNPQTLSALRKKQEKKHPKKEFSAYKSMFRNQLFQILL
 FSIIYVFLFVSLDFKEYPGYFTFYIGIFTLVSIYFSIAMYSVFYESDDV

15 Sequence description:

20 A] Length: 311 bp - 103 aa (Partial sequence)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon, no obvious signal peptide at
 N-terminus.

ID-99

25 Clone RS-78 (partial sequence)

30 TAATCTTTAGTCAACGGAGCAACAGGAAATTGCAGGCTATGCGACAGA
 TATTCCACCACATAATTAGCAGAAGTCATTGATGCTGTCGTACATGAT
 TGATCACCCCTAAAGCTAAATTAGATAAAATTAAATGGAATTCTACCTGGTCC
 AGATTTCACACTGGCGCTATCATTCAAGGAAAGATGAAATTGTAAGG
 35 CATATGAGACTGGTAAGGGGAGAGTAGCGGTTCGCTCGGAAGTGTATT
 GAAACCTTAAAGGTGGTAAGAAACAAATTATTGTTACTGAAATTCTTAT
 GAAGTTAAT

SFSQRSNRKIAGYATDIPPHNLAEVIDAVVYMDHPKAKLDKLMEFLPGPDFPT
 GAIIQGKDEIRKAYETGKGRVAVRSRTAIETLKGGKKQIIVTEIPYEVN

40 Sequence description:

A] Length: 312 bp - 104 aa (Partial sequence)
 B] No obvious Shine Dalgarno sequence or a

signal peptide. Both N- and C- termini of ORF yet to be elucidated.

5 ID-100

Clone RS-79

10 ATGGGACGTAAGTGGGCCAATATTGTTGCCAAAAAGACTGCTAAAGATGG
TGCTAACTCAAAAGTATACGCTAAATTGGTGTGAAATATGTTGCTGC
AAAGCAAGGTGAACCAGACCCCGAGTCAAACCTCAGCTCTAAATTGCTT
TGGACCGTGCTAAGCAAGCACAAGTCCAAAGCATGTTATTGATAAAGCG
15 ATTGATAAAAGCCAAGGAAACACAGATGAAACTTCGTAGAGGGACGCTA
TGAAGGTTTGGTCCAAATGGTCAATGATTATTGTGGATACTTGACATC
AAATGTTAACCGTACGGCAGCAAATGTACGTACTGCTTACGGTAAGAACG
GTGGCAATATGGGAGCTTCAGGATCGGTATCCTACTTATTGATAAAAAAG
20 GTGTCATCGTTTGCTGGTGTGATGATGCTGACACTGTCTTCGAACAATTACT
TGAAGCGGATGTAGACGTAGATGATGTTGAAGCAGAAGAGGGAAACAATA
ACAGTTTATACCGCCCCAACAGATCTCATAAAAGGTATCCAAGCACTTCGC
GATAATGGTGTAGAAGAATTCCAAGTTACTGAACTTGAAATGATTCTCAA
TCAGAAGTAGTATTGGAAGGTGATGACCTTGAAACTTTGAAAAGCTT
25 MGRKWANIVAKKTAKDGANSKVYAKFGVEIYVAAKQGEPDPESNALKFVL
DRAKQAQVPKHVIDKAIDKAKGNTDETFVEGRYEGFGPNGSMIIVDVTLSNV
NRTAANVRTAYGKNGGNMGASGSVSYLFDKKGIVFAGDDADTVFEQLLEA
DVDVDDVEAEEGTITVYTAPTDLHKGIQALRDNGVEEFQVTELEMIPQSEVVL
EGDDLETFEKL

30

Sequence description:

35 A] Length: 654 bp - 218 aa (Partial sequence)
B] Possible Shine Dalgarno sequence upstream
of ATG start, no obvious signal peptide

40 ID-101

Clone RS-80

TTGGAGAAATATTGAAGAACCCGATTACATGGATTGGATTAGTTCTTGTG
 GTTACGTGGTTTTAACTAAAAGTAGTGAATTGGTGTGTG
 TCTTGTGTTAGTATTGCTAGTCAAAGTGAT

5

MEKYLKNPITWIGLVLVVTWFLTKSSEFLIFGVCVLLLVFASQSD

10 Sequence description:

10 A] Length: 135 bp - 45 aa (partial sequence)
 B] Shine Dalgarno sequence upstream of TTG
 start codon with possible signal peptide
 evident at N-terminus.

15

20 ID-102

20 Clone RS-81

25 ATGACACAATCAGATGCATATCTCTCGTTGAACCGCGAAGACACGCTTAGA
 GATCGCACAGGTAAATTATCATTACTTCGGATAAAAGAGGCTGTTGAACAA
 TATATGATAGAACATGTTAACCTAACATACGATGGTGTTCACATCACTAATT
 GAAAAGCTAGATTATTGGTTCTAAATAACTACTATGAATCGGACCTTCTA
 AAACAATATAACCTTGAGTTATTCGCCAAATTTGAGCATGCATACGCT
 AAGAAATTGCTTTCTAAATTTATGGGGCTTAAAATTTATAATGCTT
 30 ATGCTCTTAAT

30

35 MTQSDAYLSLNAKTRFRDRTGNYHFTSDKEAVEQYMIHVEPNTMVFTSLIE
 KLDYLVSNYYESDLLKQYNLEFICQIFEHAYAKKFAFLNFMGALKFYNAYA
 LN

Sequence description:

40 A] Length: 318 bp - 106 aa (Partial sequence)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon, no obvious signal peptide

ID-103

Clone 2-11A

5

ATGGTATTATGGCAAATAAGAAAAAAACAAAAGGAAAGAAAACCAGAA
 GACCTACTAAGGCAGAAATAGAGCGTCAAAGAGCTATTCAAAGGATGATT
 ACTGCTCTGTTAACATTATTCTCTTCTTGGTATTATCAGATTAGGTA
 TTTTGGTATTACAGTCTATAACGTACATCCGTTATGGTAGGTAGCTGGC
 TTACTTATTATTGCCGCAACTTAATCTACCTTATTCTTAAATGGTG
 CGAAAGAAAGATAGCTTAGTAGCAGGTTTGATAGCTTCTTAGGATTA
 TTGATTGAGTGGCATGCTTACCTTCTCAATGCCTATTGAAAGATAAA
 GAAATTTCGCTTCAACTGCTCGATTAATTGTGTCTGATTTAATGCAATTAA
 10 AAATCACTGTTTGCCGGTGGAGGTATGTTGGGTCTTGTATTACAAGC
 CAATTGCTTTCTCTTCTAATATTGGTGCCTATATGATTGGTCTCTTC
 ATCATTGTTGGTCTCTTTAATGAGTTCTCTGGAAAGTTATGACATCGTCG
 AATTATTAGAGCTTTAAAAATAAAGTGGCAGAGAAGCACGAGCAAAAT
 15 AAAAAGGAGCGTTGCTAAGCGAGAGATGAAAAAAGCAATCGCTGAACA
 AGAGCGCATAGAGCGTCAAAAAGCTGAAGAAGAAGCTTATTAGCTTCGG
 TTAATGTAGACCCCTGAAACGGGTGAGATTCTAGAGGATCAAGCTGAGGAC
 AATTGGATGATGCGCTACCACCTGAGGTAAGTGAACACATCAACTCCGGT
 ATTTGAGCCAGAGATCCTGCTTATGAGACATCGCCTCAAAATGATCCTT
 20 ACCAGTAGAGCCGACAATTATTAGAAGACTATGATTGCCGATTCTAA
 TATGAGAGAAAATGATGAGGAAATGGTTATGATTAGATGATGATGTTAG
 ATGATAGTGTATAGAAAATGTCGACTTACACCTAAAACGACACTGGTT
 ATAAATTACCAACGATAGATTATTGCACCAAGATAAGCCTAAAATCAAT
 CCAAAGAAAAGGATTAGTCCGAAAGAATATCAGAGTTTAGAAGAAACA
 25 TTTAGAAGTTGGTATCGATGTAAGTAGAACGTGCTGAAATTGGACCA
 TCAGTTACTAAATATGAAATTAAACCAAGCAGTTGGAGTTCGTGTGAATCGT
 ATTTCAAATCTATCTGACGACCTAGCTCTGCTCTGCAGCAAAAGATGTG
 CGTATAGAACGACCAATTCTGGAAAATCATTAAATAGGTATTGAAGTTCCT
 AACTCAGAAATTGCAACGGTTCTTCCCGCAACTTGGGAACAATCTGAT
 30 GCCAATCCTGAAAACCTTTAGAAGTACCACTAGGAAAAGCTGTTAACGG
 CAATGCTCGCAGTTAACCTAGCTAGATAATGCCGCATCTTGGTAGCTGG
 TTCAACTGGTCAGGTAAATCTGTGGCAGTTAATGGAATTATTCAAGTAT
 TTTGATGAAGGCACGTCAGATCAAGTTAAGTTATGATGATTGATCCCAA
 AATGGTTGAATTATCTGTTATAATGATATTCCACATTATTAATCCCTGTT
 35 GTAACCAATCCCGTAAAGCAAGTAAGGCACCTCCAAAAAGTTGTTGATGA
 40 AATGGAAAATCGATACGAGTTATTAGCAAAATTGGTGTGCGTAATATAG
 CAGGTTATAATACAAAGGTTGAAGAGTTAATGCTCCTCTGAGCAAAAC
 AAATGCCTTGCCTTAATCGTTGTCAATTGATGAAATTGGCTGACTTGAT
 GATGGTTGCTAGTAAAGAAGTTGAAGATGCTATTATCGTTGGGGCAAAA
 AGCACGTGCTGCAGGTATCCATATGATTCTGCAACTCAACGTCCATCCGT

AGATGTTATTCGGTTGATTAAGCAAATGTTCCGTCGCGTATTGCATTT
 GCTGTTCAAGTGGTACTGATAGCCGTACGATCCTTGATGAAAATGGTGCT
 GAAAAGCTCTGGGACGGGGTACATGCTCTTAAGCCTATTGATGAGAAT
 5 CATCCAGTACGACTACAAGGTTCTTATTCAGATGATGATGTTGAAAGG
 ATCGTTGGTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTT
 GATCCTGGAGAAGTATCTGAAACAGATAACGGCTCTGGTGGTGGCGCGG
 ACTACCTGAAAGTATCCTCTTTGAAGAAGCCAAGGGACTCGTTTAGA
 GACGCAAAAAGCAAGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTT
 10 CAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTG
 GTCCAGCAGAAGGAACCAAGCCACGAAAAGTTTAATGACTCCAACCTCG
 AGTGAATAA

 MVFMANKKTKGKKRPTKAEIERQRAIQRMITALVLTILFFGIIRLGIFGIT
 VYNVIRFMVGLAYLFIAATLIYLYFFKWLRLKDKDSLVAGFLIASLGLLIEWHA
 15 YLFMMPILKDKEILRSTARLIVSDLMQFKITVFAAGGMLGALIYKPIAFLFSNIG
 AYMIGVLFILGLFLMSSLEVYDIVEFIRAFKNVAEKHEQNKKERFAKREMK
 KAIAEQERIERQKAEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETST
 PVFEPEILAYETSPQNDPLPVEPTIYLEDYDSPNMRNDEEMVYDLDDDVDD
 20 SDIENVDFTPKTLVYKLPTIDLFPDKPKNQSKEKDLVRKNIRVLEETFRSGI
 DVKVERAEIGPSVTKYEIKPAVGVRVNRISNLSDDLALALAACKDVRIEAPIPGK
 SLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPH
 LLVAGSTGSGKSVAVNGISSLMKARPQVKFMMIDPKMVELSVYNDIPHLLI
 PVVTNPRKASKALQKVVDENRYELFSKIGVRNIAGYNTKVEEFNASSEQK
 25 QMPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVD
 VISGLIKANVPSRIAFAVSSGTDTSRILDENGAEKLLGRGDMLFKPIDENHPVRL
 QGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGGGGGVPESDPL
 FEEAKGLVLETQKASASMIQRRLSVGPNRATRLMEELEAAGVIGPAEGTKPRK
 VLMTPTPSE*

30
 Sequence description:

35 A] Length: 2451 bp - 817 aa (Full-length gene)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon, possesses a potential signal
 peptide

40 ID-104

Clone 2-18/22b

ATGTCACAAGAGCAAGGAAAAATTATATTGTAGAAGATGATATGACGAT
 TGTGTCACTTTAAAAGATCATTATCAGCTAGCTATCATGTCTCTAGTGTG
 AGCAAATTCGATGTGAAACAAGAAATTATCGCATTCAACCCGATTG
 5 ATACTAATGGATATTACGTTACCCATTAAATGGTTTACTGGACTGCAG
 AATTGCGTAAGTTTAACAATTCTATTATTCATCTAGTAATGA
 TGAAATGGATATGGTTATGGCATTAAATATGGGGGTGATGACTTTATTTC
 AAAACCATTCTCTAGCTATTAGATGCTAAGCTAACTGCTATTAAAG
 GAGAAGTCAACAAATTATCCAACAGGAATTAACTTTGGGGATTACGTT
 GACAAGAGAAGGGTTATTGTCTAGCCAAGATAAAGAGGTATTATTCATGC
 10 CAACAGAAAATAACCTATCTATCTTGCTCATGCATCCTAAACAAGTAG
 TCTCAAAAGAGTCTCTATTAGAGAACTTGGAAAATGATAGTTTATTG
 ATCAAAATACACTTAATGTTAATATGACACGCTACGTAAAAAAATTGTCC
 CAATAGTTTGATTACATTACAGTGAGAGGAGTTGGTATTACTAC
 AATGA
 15

MSQEQQKIVIEDDMTIVSLLKDHSASYHVSSVSNFRDVKQEIIAFQPDILM
 DITLPYFNGFYWTAELRKFLTIPIIFISSNDEMDMVMALNMGGDDFISKPFSLA
 VLDAKLTAILRRSQQFQQELTFGGFTLTREGLLSSQDKEVILSPTENKILSILLM
 20 HPKQVVSKESLLEKLWENDSFIDQNTLNVNMTRLRKIVPIGFDYIHTVRGVG
 YLLQ*

25 Sequence description:
 A] Length: 669 bp - 223 aa (full-length gene
 sequence)
 B] Shine Dalgarno sequence present upstream of a GTG start codon.
 Was not identified directly by LEEP. This gene was found upstream of
 30 gene ID-10 described in WO 00/06736.

ID-105
 35 Clone 2-20

ATGTATCAAACCTCAGACAAATAAGGAAAAATTGTTTATTTGAAATT
 TTTATCCCAGTATTGATTATCAATTGCTAATTTCAGCTACTTTATTGA
 40 TTCGGTTATGACTGGACAGTATAGTCAGCTACATTGGCAGGTGTCAAC
 TGCTAGTAATTATGGACTCCGTTTCGCTTATTAGTAGGTATGATTCA
 GCATTAGTACCACTAGTTGGTCAACATTGGTAGAGGAAATAAAGAAC
 AATTCCGACAGAATTCAATTCTATATTAGTTGATACTGTCCTTA
 ATATTATTTAATCATGCAATTATTGCTCAACCTGTCTGGGAGTTGG

GTTAGAAGATGAAGTCTAGCAGTGGCGTGGTTATTTAAATTATATGT
 TGATTGGAATCATGCCGCTGGTGTTCAGCATTGCCGTCATTCTTGAT
 TGCATTGGGTTAACAAAGGTTATCTATGTATCTGATGCTTTAATTCTACCC
 5 TTAATTCACTTTAATTATATGCTTACGGTAAATTGGTATGCCTA
 GACTAGGAGGTGCGGGGGCAGGTCTTGAACCTCTTAACCTATTGGGCTA
 TTTTATTGGTATTATTGTGATGTCACTCATCCTCAAATTAAACATA
 TCATATATGGACTCTGGAAAGAATAAAAGCTCCTTGATTATTGAAGATAT
 TCGATTGGGATTACCGATTGGTTACAAATTTCAGAAGTTGCAATT
 10 GCAGTAGTAGGCTTATTCAATGGCAAAATTTCCTCAATCATTATTGCAGCA
 CATCAGGCTGCTATGAATTTCATCATTAAATGTATGCATTCCCTTAAGTA
 TTTCCACTGCTCTAGCTATTACAATATCGTTGAAGTAGGGCAGAGCGCT
 TTCAGGACGCAACCACCTATAGTAGGATAGGACGCTAACAGCGTAGGG
 ATTACATCAGGAACCTACTATTTCATTTCGTGAGAATGTAGCAG
 15 CAATGTATAATAGTCCCCCTCACTTGTGCTATTACAGCTAACCTCAAC
 TTATAGTCTCTTTCCAGTTGCAGATGCTTATGCAGCTCCTGTACAGGGG
 ATTTACGAGGCTATAAGGATACAACAAAACCATTATGATCGGTGCGGG
 CTCTTATTGGTTATGTGCTTGCCTATTGGATTGGTTAACACAGGTATT
 CCAGTTAGGTCCGTTGCCTATTGGATTGGTTAACACAGGTATT
 20 TGTGGTCTATTCTAAACCAACGTCTGCAAAAGATTAAGAAGTTGTATTAT
 TAA

 MYQTQTNKEKFVFLKLFIPIVLIYQFANFSATFIDSVMTGQYSQLHLGVSTAS
 NLWTPFFALLVGMISALVPVVGQHLGRGNKEQIRTEFHQFLYGLLILSLIFL
 MQFIAQPVLGSLGLEDEVLAVERGRGYLNMLIGIMPLVLSICRSFFDALGLTRL
 25 SMYLMLLILPFNSFFNYMLIYGKFGMPRLGGAGAGLGTSLTYWAIFIGIIIVMS
 LHPQIKTYHIWTLERIKAPLIIEDIRLGLPIGLQIFAEVAIFAVVGLFMAKFSSIIIA
 AHQAAMNFSSLMYAPPLSISTALAITISFEVGAERFQDATTYSRIGRLTAVGITS
 GTLLFLFLFRENVAAMYNSAPHVAITAQFLTYSLFFQFADAYAAPVQGILRG
 30 YKDTTKPFMIGAGSYWLCAALPLAVILEKNSQLGPFAWIGLITGIFVCGFLNQ
 RLQKIKKLYY*

Sequence description:

35 A] Length: 1341 bp - 447 aa (full length gene)
 B] Shine-Dalgarno sequence present upstream of
 ATG start codon, There is a potential signal
 peptide sequence

40

Clone 2-4A

5 TTGCTAGTTCTCTAGTTCTGTCATTTCTGTCATTCGTCGTT
 GTCTTCATCAACACGAAATAAGTCTATAAACTATCAAATAATTCATAGA
 CTTATTATATCAATTTCATAAAAATGCTATAATAAAAACCATGTCATTTCA
 TTAAAAAATTAGAAATCCATACGGTGAACATACCGTAAAGAAACTCCTTGA
 AGATTATTTTGATTCCACGTAAGATTAGACATTGGCTGTTAAAAAA
 10 CATGTAATTAAACAATGAATTCTTAATTGGCAAACGTGCGTCCAAGAA
 AACGATACTATTACCTTAATCTTGATGATGAGGATTACCCACTAAAAAA
 ATTCCTCTGGGCAGAGCAGAGCTTATTGATTGTCTTATGAGGATGAACAT
 CTTATTATCGTTAATAAACCTGAAGGTATGAAAACTCACGTAACCAACCA
 AATGAAAATAGCACTGTTAAATCATGTATCTGCCTATTCTGGACAAACATGC
 15 TATGTTGTCATCGCCTAGATATGGAGACCAGTGGAGCTGTTTATTGCT
 AAAAATCCATTATACCTCCCTTATCAATCAACGCTTAGAACGAAAAGAA
 ATTTGGCGTGAATATTGGCTTATTGAGGAAAATTTCACCTAACGAT
 CAAGTTTGAGAGACAAAATTGGACGGAACCGTCATGACAGACGTAACG
 AATCATTGATTCTAAAAACGGTCAACATGCTATGACAATCATTGACGTTT
 20 GAAGTATATCCAAAATAGTAGTCTCATAAAATGCCGACTGGAAACCGGAA
 GAACCCATCAAATTCCGATTCACTTATCTCATCACGGACATCCTTAATAG
 GAGATCCCCTCTACAACCCCTTCTTAATAATGAAAGGTTAATGCTACACG
 CTCACCGATTGACTCTATCCCATCCATTAACTTGCAGAAACTATTAGCGTAG
 AGGCCCTTCATCTACTTCGAGAAGGTTAAACAATTATAAAAAGGAG
 25 TTGGATAA

 MLVSSLVSCSFFLVISSLSSSTRNKSINLSNNFIDLLYQFSIKCYNKTMFSLKR
 NPYGEHTVKELLEDYFLIPRKIRHFLRVKKHVLINNEFINWQTVQENDTITLIF
 30 DDEDYPTKKIPLGRAELIDCLYEDEHLLIVNKPEGMKTHGNQPNEIALLNHVSA
 YSGQTCYVVHRLDMETSGAVLFAKNPFLINQRLERKEIWREYVALVEGKF
 SPKHQVLRDKIGRNRHRRKRIIDSKNGQHAMTIIDVLKYIQNSSLIKCRLETG
 RTHQIRIHLSHHGHPLIGDPLYNPSSNNERLMLHAHRLTLSHPLTCETISVEAPS
 STFEKVLNNYKKGVG*

35 Sequence description:
 40 A] Length: 1029 bp - 343 aa (Full length gene sequence)
 B] No obvious Shine-Dalgarno sequence upstream
 of the putative TTG start codon. Possesses a
 potential leader peptide sequence.

ID-107

Clone 2-54

5

10 GAACTAAATGCAACTAACCTAATAATAGAACTACCTATAATTACCCGAA
 AGCAGTCATTCCATTGCAGAACACAGAGATTCTGTAGAATCAAAGGG
 TTCTCGGTTGCATTACTTAATAGCGATGAATTAGAAAGACAGCGGGAGA
 GGATAGAGGTTTGAAAGGGATAAGTTGAGGTCTTGGATATCATTCTAA
 GGGAGATTATCGACAAGTAATGTCATAGGTAAATACGGACATTGCTAGTC
 AGATATCGTGGGCTTAAAAAGAACATGCGATGCAGGAACACCATCTTACT
 AAAACATTCTCTCAAAAGGATGGAAAGTTATCGTCTGTTATAGAGGGGAT
 GCTTGCTATTGGCAAAGAGAAAGTAGAGAAAGAAATAAAATATAGGGTA
 15 ATTTATGGCAAAAATTAAAGCTAAGGCACACTGCCTGTTGCTGTGTTG
 ATAATTGAATTGAAAGATATAAAATCTTATTTCATATTATTGTCATCT
 AAACCATCAGCTCAAATTACCTAAAGGTGCTACTTCTGCTAAACAGA
 AGTATATAGGGGAGGAGATTGGGAGAAAAAAATAAGATAATGTGTTG
 GTTACCGTATCCCCTCATTATTGAAAACCCAAAAGGAACTTACTGCGG
 20 GAGCTGATGAAAGAATTGAGCAAGCTTGTGATTGGGGAAACATAGGAATG
 GTTATTCGCCGTAGTGAGGATGATGGTGTCACTGGGAAAAAGAGAAAC
 TATTGTCATCTCCGTAAATAACCCCTAGAGTCCGCTAGTTACTAGTGGTGA
 CTATAGTGGCTCACCTATTAAATATGGATATGGCATTAGTTCAAGATACTAG
 CTCCAAGACGAAACGTATTTTCAATATATGATATGTTCCAGAAGGAAG
 25 AGGCATTATTAGTATTGCTAACACACCTGAAAAAGAACATACCCAAATCG
 GAGGACAGTCTTATCTAATTATATAATAATGGAAAGAACATCGAAGGTTT
 TTACTATCCGTACAAAGGTATTGTATATAATTAAAGGGAAAAAGACTG
 ATTATCATGTTATAACAGAAACTACTAAAAGTGACCATTCAAATCTAGGGG
 ATATTATAAGGGAAAACAGCTACTGGAAATATATATTTCACAAACATA
 30 AAACGTCACCATTGTTAGCAAAATCAAGCTATGTGTGGATGTCATATA
 GCGATGATGATGGTAGGACATGGTCATCACCTAGAGATATAACAGCAAGT
 CTTCGTCAGAAAGGCATGAAATTGGAAATGGACCTGGAAGGGTAT
 AGTTTAAAATGGGGCCACACGCTGGTGTATTATTATTCCCTGCCTATTCT
 ACGAATTGAAATCTCATCTAACAGAGGTTACAATCTCACGCCCTAATTAT
 35 TCAGACGACCATTGGAAAAACGTGGCATACTGGAAAAGCAGTTAATGATAA
 CCGTATACTTCTAATGGTAAAAAAATTCACTCCTAACATGGATAATAA
 AAAAGAACAAAATACAGAACCGTACCCGTTCAATTGAAAAATGGGACA
 TTAAGTTATTATGAGGAATCTAACTGGTAACCTAGAAGTAGCCACAAGTA
 AAGACGGCGGGGAGACTGGCAAAACCATGTTAACACGATATAAGGAAATT
 40 CATGATGCTTACGTCCAACATCAGCTATTGCTTGAGCATGACAAAAAA
 GAGTATATTATTAGTGAATGCTAATGGGCCAGGGAAAGAAGTGCCAAGA
 TGGATATGCACGTCTAGCGCAAGTTAACGAAATGGTAGTTAAGTGGTT
 ATATCACCACATTCAAGATGGTCTTACAACACTGTTCAACA
 ACTTAATAATGATCAATTGGTGTCTTATGAACATAGAGAAAACATCA

AAATAGTTTACTTAAATTACAAAGTTTAATTGGAGTTCTTAGCAA
 AATACAGAGAAGCAAGGCACTTATGGGAGAAAATGGCAGCAAATTGGCA
 TGTTTGTAAATTATTAATG

5 ELNATQPNNRTTYIPESSHISIAEQQRFLIESKGSSVALLNSDEFRKTAGEDRGF
 ERDKLRSLDIIPKGDLSTSIVGNTDIASQISLGFKKNAMQEHHLTKTFSQKDG
 KLSSVIEGMLAIGKEKVEKEIKYSGNLWQKLAKAHCLVCCVDNLNFEDIKS
 10 YFQYYCHLNHQLKLPKGAILSAKTEVYRGDFGRKNKDNVFGYRIPSLKTQ
 KGTLLAGADERIEQACDWGNIGMVIIRRSEDDGVTWGKRETIVNLRNNPVPVL
 VTSGDYSGSPINMDMALVQDTSSKTKRIFSIYDMFPEGRGVISIANTPEKEYTQI
 GGQSYLNLYNNNGKSKVFTIRDKGIVYNFKGKTDYHVITETTKSDHSNLGDI
 15 YKGKQLLNIYFTKHKTSPFRLAKSSYVWMSYSDDDGRTWSSPRDITASLRQ
 KGMKFLGIGPGKGIVLKWGPHAGRIIPAYSTNWKSHLRGSQSSRLIYSDDHG
 KTWHTGKAVNDNRILSNGEKIHSLTMDNKKEQNTESVPVQLKNGDIKLFMRN
 LTGNLEVATSKDGGETWQNHVKRYKEIHDAYVQLSAIRFEHDKEYILLVNA
 NGPGKKCQDGYARLAQVNRNGSFKWLYHHIQDGSFAYNSVQQLNNDQFG
 20 VLYEHREKHQNSFTLNYKVFNWSFLSQNTEKQGTLWEKMAANWHVLFKFYL
 *

20 Sequence description:

A] Length: 2052 bp - 684 aa (partial gene sequence)
 B] N-terminus has yet to be determined

25 ID-108

30 Clone 2-61

ATGCCTAAATTAAATCGTATCTTCCTCTGCATTTATTATCCCTGACTTGTG
 35 TAAACTCTGTGCAAGCTGAAGAACATAAAAGATATTATGCAAATTACCGA
 GAAGCCGGATATGATGTTAAAGATATTAAATAAAACCTAAAGCGTCTATCGTT
 ATTGACAATAAAAGGTCAATTGTGGAGAGATAACGCCGATTAGAACGT
 GATCCCGCTAGCATGTCTAAATGTTACTTTATATTACTATTGAAGACT
 40 TAGCTAAAGGAAAAACAAACCTAACACACCACAGTGACTGCAACAGAAACA
 GACCAAGCCATAAGTAAGATTATGAAATTAGTAATAACAATATTATGCT
 GGGGTTGCTTATCCTATTCTGAACGTGATTACTATGACGGCTGTCCCGTCA
 TCTAATGTAGCAACTATTATGATTGCTAACCAACTATCACAAAACAATCCT
 GACGCCTTATTAAACGAATCAATGAAACCGCCAAGAAACTCGGTATGAC
 AAAAACACTCACTTTATAACCCCAGTGGGGCGGTAGCGAGTGCTTTAATGG
 ACTTTACTCCCCAAAAGAATACGATAACAAATGCTACTAACGTTACGACTGC

5 ACGTGATCTATCAATTAAACCTATCATTCTTAAAAAATACCTGATATA
 CTGAACATACAAAATATCCTGAAGTCAAGGCCATGGTCGGAACCTCTTAT
 GAAGAAACATTACAACCTATAACTACTCTACCCCCGGCGCTAAATTGGA
 TTAGAAGGAGTAGATGGCTAAAAACTGGTCTAGCCCTAGCGCTGCTTT
 AATGCCTTAGTTACAGCTAACGCCAGAATACTCGCTGATAACTGTGGTT
 TTAGGAGTTGGCGATTGGTCAGACCAAGACGGAGAGTACTATCGTCATCC
 GTTGTCACGCTCTGTAGAAAAAGGTTAAAGACGCTAAAAATATTTC
 TTCTAAAACCTCTGTATTAAAAGCCGTTAACCTAAAAAGAAGTTACTAA
 AACCAAAACTAAATCTATTCAAGAACAGCCTCAAACAAAAGAACAGTGGT
 GGACAAAAACAGATCAATTATCCAATCACATTGTATCTATTAAATTG
 TTCTGGGCACCATCGCTAGCCTTGTCTTAGCTGGATAGTATTACTTAT
 AAAGCGCTCTAGATAA

 15 MPKLIVSFLCILLSLCVNSVQAEEHKDIMQITREAGYDVKDINKPKASIVIDN
 KGHILWEDNADLERDPASMSKMFPLYLLFEDLAKGKTNLNTVTATETDQAI
 SKIYEISNNNIHAGVAYPIRELITMTAVPSSNVATIMIANHLSQNNPDAFIKRINE
 TAKKLGMTKTHFYNPSGAVASAFNGLYSPKEYDNNATNVTTARDLISILTYHF
 LKKYPDILNYTKYPEVKAMVGTPYEETFTTYNYSTPGAKFGLEGVDGLKTGS
 SPSAAFNALVTAKRQNTRLITVVLGVGDWSDQDGEYRHPFVNALVEKGFK
 20 DAKNISSKTPVLKAVKPKKEVTKTKTSIQEQPQTKEQWWTKTDQFIQSHFVS
 ILIVLGTIASLCLLAGIVLLIKRSR*

25 Sequence description:

30 A] Length: 1188 bp - 396 aa (full length gene)
 B] Shine Dalgarno sequence present upstream of
 ATG start codon, possesses a potential signal
 peptide

35 ID-109

 Clone 45

40 ATGACTGAAAAATTATAATTGGCAACGCTTGGAACCGGGCGTTATTGCC
 AACGAATTAGCCCAAGCACTGGAAAGCACGTGGACAAAAATTATATTCTGT
 AGCTAATAGAACTACGACAAAGGACTTGAATTGCTAACAAATATGGTA
 TCCAAAAAGTTATGATCACATAGATCAAGTATTGAAGACCCCTGAAGTGG
 ATATCATTATCTACTCCCCACAATACTCACATCTCATTACGAAA

GGCTTAGCAAATGGTAAGCACGTTCTTGCAGAAAATCTATTACTTAAA
TAGTACTGAGCTAAAGAACGCATAGATTAGCCGAAACTAACCATGTTGT
CTTAGCTGAAGCCATGACTATTTCATATGCCAATTACCGCCAATTAAA
AACATTAGTTGATAGGGAAAATTAGGACCGTTAAAATGATTCAAATGA
5 ATTTCGGAAGTTATAAAGAACATGATATGACTAACCGTTTCAGTCGTG
ACCTAGCAGGCAGGTCTTGCTGGACATTGGTGTATGCACTTCTGTAT
TCGCTGGTTATGTCAGAACGACCTCACAAACATTACCTCTCAAGTTACATT
TGCACCAACAGGGTTGATGAACAAGTTGGTATCCTACTAACCAACCCAG
CAAATGAGATGGCGACTGTCAGCCTAGTTACATGCAAAACAAACCTAAA
10 CGAGCAACTATCGCTACGATAAAGGCTACATTGAACCTTTGAATATCCG
CGAGGACAAAAGGCAGTTACTTACTGAGGATGGGCATCAAGATAT
TATCGAAGCTGGCAAAACTGAAAATGCTCTCCAATATGAGGTAGCTGATA
TGGAAAGAACCCATTTCAGGAAAAACTAACCACATGTAACCTAAACTATACC
15 AAAGATGTTATGGATATCATGACACAGCTACGTCAAGAATGGGGATTAC
CTACCCAGAAGAAGAAAAATGA

MTEKYYNWATLGTGVIANELAQALEARGQKLYSVANRTYDKGLEFANKYGI
QKVYDHIDQVFEDPEVDIYISTPHNTHISFLRKALANGKHLCEKSITLNTEL
20 KEAIDLAEVNHLAEAMTIFHMPIYRQLKTLVDSGKLGPLKMIQMNFGSYK
EYDMTNRFFSRDLAGGALLDIGVYALSCIRWMSEAPHNITSQVTFAPTGVDE
QVGILLTNPANEMATVSLSLHAKQPKRATIAYDKGYIELFEYPRGQKAVITYT
EDGHQDIIEAGKTENALQYEVADMEEAISGKTNHMYLNYTKDVMIDMTQLR
QEWGFTYPEEEK*

25

Sequence description:

30

- A] Length: 984 bp - 328 aa (full length gene)
- B] Shine Dalgarno sequence present upstream of ATG start codon, possesses a potential signal peptide

35

ID-110

Clone 2-2

40

GTGTATTCTCCTGTTAAATCTTCTAAAGGAAAAGTGTATTGTTAAAAAGT
GATTTCTAAAGAGCTCATAGAAAGGAGAGGAAATATTGTTT
MYSPVKSSKGKVILLKSDFLKSFERRGNICF

Sequence description:

5 A] Length: 96 bp - 32 aa (partial sequence)
 B] GTG start codon - no obvious Shine-Dalgarno
 sequence
 Possesses a potential signal peptide

10

ID-111

15 Clone 2-3

AAATACTGTATCATTGCAACCTCAAATGCAGGTTTGGAAACGAAGCATT
 20 ACAGGTGACAGCGATAAAGACTGAAAATTATGGAACGAATTCTCCATA
 TTTCCCGTCCAGAATTCTAAATCGTTCAATGGTGTATTGAATTCTCTCAC
 CTAACGAAAGATGACTTAAGCGAAATTGTAGATTGATGCTGATGAAGTT
 AACCAAACAATTGGCAAAAAAGGAATTGACCTTGTGGTAGATGAAAATGT
 TAAATCACACTTAATTGAACTGGTTATGACGAAGCAATGGGAGTACGTC
 CATTGCGCCGTGTCATCGAGCAAGAAATTGAGATCGCATCACAGACTACT
 25 ATCTCGATCATACAGACGTTAACACCTAAAAGCTAATTGCAAGATGGCC
 AAATCGTCATTCTGAAAGATAA

KYCIIATSNAGFGNEAFTGDSDKDLKIMERISPYFRPEFLNRNGVIEFSHLSKD
 30 DLSEIVDMLDEVNQTIGKKGIDLVVDENVKSHLIELGYDEAMGVRPLRRVIE
 QEIRDRITDYYLDHTDVKHLKANLQDGQIVISER*

Sequence description:

35 A] Length: 429 bp - 143 aa (partial sequence)
 B] N-terminus yet to be elucidated. This gene
 was not in frame with nuc

40

ID-112

Clone 2-5

ATGTCAATGAATTTCATTTACCAACATATTGGCCTATTTAATTATG
 GTGTGATGGTAACCATTATGATTCAACATGTGTTTTTTGGAACTAT
 TATAGCGTGTAAATTGCTTAGTAAAGCGTACTAATTACATTTCTCACA
 5 ATATTAGCTAATTCTATGTATGGGTATTCGTGGGACACCGATGGTAGTT
 CAAATTATGATTGCTTCGCATGGATGCATTAAACAATTACCAACAATT
 AGCTTGGTGTAGATTAGATTACACGACTTACCTGGTATCATTATCATT
 10 TCATTTCCTAAATAGTGGTGCCTATATTGGAAATTGTACGTGCAGGGA
 TTGAGGCTGTACCATCTGGACAAATAGAAGCAGCTTACTCGTTGGGATT
 GACCTAAAAAACACTTCGCTATGTTATCTTACCCCAAGCTTTAAAAATA
 TTTTACCTGCTCTAGGAAATGAATTATTACAATTAAAGATAGTGCCTCT
 15 CCTTCAAACATTGGTGTATGGAATTATGGAACGGAGCACAATCAGTTGT
 AACGGCTACTTACTCACCAGTTGCACCGTTATTATTGCAGCATTACTAT
 TTAATGTTGACAACGATTCTCTCAGCTTGTAAAACAAATGGAGAAATAT
 CTTGGGAAAGGGTAAAAATAGATGGTTGA
 20 MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTIL
 ANFYVWVFRGTPMVVQIMIAFWMHFNNLPTISFGVLDLDFTRLLPGIIIISLN
 GAYISEIVRAGIEAVPSGQIEAAASLGIRPKNTLRYVILPQAFKNILPALGNEFITI
 IKDSALLQTIGVMELWNGAQSVVTATYSPVAPLLFAAFYYLMLTILSALLKQ
 MEKYLGKGVKIDG*

25 Sequence description:
 A] Length: 699 bp - 233 aa (full length gene)
 B] Shine-Dalgarno sequence preceded the 'ATG'
 start codon. Possesses a potential leader peptide
 sequence.
 30

ID-113
 35 Clone 2-7
 40 ATGAAAGACCTATTACGAAATAGTCTAGAGCAAAGTGGAAATTAAAGTTT
 TCAAGATATGATTACATATTCTTGTAGCAGCTTATTGAGTGTAGTTATT
 TATGTTCTATGCTTACCGATAGTGGAACTGCCTATAGTAAAAAGTTT
 AATGTTCTATTAAATGACATTGACGGTCTGACTGCAACAGTAATGACCGTT
 ATTGGTAATAATGTAGCCTTGTCAATTGGGTATGGTCGGTGCCCTGTCAGTT
 GTTCGTTAGGACAGCCATAAAAGATTCAAGAGAGACAGTTATTTTT
 TGGACCATAGTTGTTGGTATCTGTTGTTGACTATGTGGTAGCT

5 GCATTAGGAAGTAGCGTTATCTTATTATGGGTTATGGGACGTGTT
 AAAAACGAGAATCGTATGTTATTGATTGTGAAGTGCAGATAAACACTAGA
 AGTTGATTAGAAGGAATTCTTCCAATATTTGACGGAAAAGCTGTTCA
 GCGTGTAAAAATTCAACAACTAATACTATTGAAATGATTTCGAAATCTC
 TAGAAAAGATTACGATAAGCAACTCCATGTAGATAATCAGTTAAGTGAAA
 AAGTGTACCAATTGGGAAATATTGATTATTCAACATTGTTAGCCAAAGCG
 ACGAAATCAATGGGTAG

10 MKDLLRNSLEQSGNLSQDMILHILVAALLSVVIYVSYAYTHSGTAYSKKFNV
 SLMTLTVLTATVMTVIGNNVALSLGMVGALSVVRFRTAIKDSRDTVYIFWTIV
 VGICCGVGDYVVAALGSSVIFILLWVMGRVKNEENRMLLIVKCDRTLEVDLEGI
 FFQYFDGKAVQRVKNSTNTIEMIFEISRKDYDKQLHVDNQLTEKVYQLGNID
 YFNIVSQSDEING*

15 Sequence description:

20 A] Length: 678 bp - 226 aa (full-length gene)
 B] ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide sequence

25 ID-114

Clone 2-8

30 AAAAATTCACTTCTAGATTCACTTACGACTATATACTCAGAAGTACCAAAC
 CTAATCCAAGGTTGAAAAAAGAAAGAAGGAAGTCAGTATGACAAACTAT
 AAAAACAACTTAAAGATGAGGCTATACGTGTTGAAGAGAGACAACAAAAGA
 ATCATTTACGATGTTGATATTGCCTTGTTCAGCTGGTGGATCTATTCA
 GCAAAGTTCGCTCCTTATGCAGTAAAGTCTGGAGCAGTTGTTAGATAAAC
 35 ACGTCATATTTCGTCAGAACCTGATGTTCCACTAGTTGTTCTGAAGTAA
 ATGCTCATGCCATGATTGGTCATAATGGTATCATAGCTTGTCCCAATTGTT
 TACTATTCAAATGATGATTGCTTAGAGCCCATTCTGTCAAAAATGGGGGAT
 AGAGCGTGTATAGTTCCACCTATCAAGCTGTTCGGGTTCAGGTGCACG
 TGCTGTTGAAGAAACTAAGGAACAGTTGAGACAAGTTT
 40 KFILDSFYDYILRSTKPNPRFEKRKKEVSMTNYKNNFKDEAIRVEETKESFYD
 VDIALFSAGGSISAKFAPYAVKSGAVVVDNTSYFRQNPDVPLVVPEVNAHAMI
 GHNGIIACPNCSTIQMMIALEPIRKWGIERVIVSTYQAVSGSGARAVEETKEQ
 LRQV

Sequence description:

5 A] Length: 499 bp - 165 aa (partial sequence)
 B] N-terminus has yet to be determined

10 ID-115

15 Clone 2-9

20 ATGACAAATGAATTGATAATGCAAGCTTTGAGTGGTATTACCTAGTGAT
 GGGAATCACTGGAAGAAATTAGAGGAGTCTATATCAGACCTTAAAAAACT
 TGGATTAGTAAAATCTGGTTACCACCAAGCATTAAAGGAACTAGCAGTG
 ATGATGTAGGATATGGTGTATGATCTCTTGATTAGGAGAATTGACC
 AGAATGGAACAATTAGAACAAAATATGGTAGGAAAGAAGAGTATCTAAA
 GCTTATTAAGTCGTTAAAGGCAAATGGCATTAAACCGTTGCAGATATCGT
 TCTTAACCATAAAGCCAATGGTGATCATAAAGAAAAATTCAAGTCATCA
 AAGTCAATCCTGAAAATCGTCAAGAACGCATTAAGTGAACCCCTATGAGATT
 GAAGGATGGACGGGATTGATTCCAGGTAGACAGGGTGAGTACAATGA
 TTTT

25 MTNELIMQAFEWYLPSDLGNHWKKLEESISDLKKLGISKIWLPPAFKGTSDDV
 GYGVYDLFDLGEFDQNGTIRTKYGRKEEYLKLIKSLKANGIKPFADIVLNHKA
 NGDHKEKFQVIKVNPNRQEALSEPYIEGWTGFDFPGRQGEYNDF

30 Sequence description:

35 A] Length: 456 bp - 152 aa (partial sequence)
 B] ATG start codon is preceded by a Shine-Dalgarno sequence, no leader peptide sequence.

40 ID-116

Clone 2-10

ATGGAGGTTCTTATGAAGAAAGTGTAGTAAGTAGCTTTGGTTAGGG
 ATTACGATAACGTTACAACCAGTAGTTGAGGCTAAGGGGCAAAAGTAGC
 TTATACACAAAGAGGGAATGACTGCTCTTCGGACACAAATAAAGATAAAG
 5 TCACTACTATTCTATTGACGAGATTCAAAAAAGCTAGAAGGTAAGAAGC
 CGATTACTGTTAGTTGATATTGATGATACACTGCTTTCACTAGTCATA
 TTTCAATATGGTAAAGAATATGTAACTCCTGGATCGTTGATTTCTCAT
 AAACAAAAATTCTGGATCTGTTGCAAAACGAGGAGATCAAGATTCCAT
 10 TCCCAAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAACGAGGAG
 ATAAAATTGTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAG
 GGCAGGTTGATAAAACAGCTAAAGCCTAGCTAAAGATTAAATTGTA
 CCATCTGAT

MEVLMKKVLVSSLLVLGITITLQPVVEAKGPKVAYTQEGMTALSDTNKDKVT
 15 TISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQYGKEYVTPGSFDFLHKQKFW
 DLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGSMYKEGEVDKTA
 KALAKDFKFVPSD

20 Sequence description:
 A] Length: 516 bp - 172 aa (partial sequence)
 B] ATG start codon is preceded by a Shine-Dalgarno sequence, Possesses a leader peptide sequence.
 25

20 ID-117

30 Clone 2-17

ATGCTTAAAGATTATTACTGAAGATGGGAATTGACAAAGATTAGTCGT
 35 CGTTCTGTTGGATGTTAGTGGTTATCTATTGTCTTATTATTGTCAGGATGT
 GTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTCAGC
 GCTTCGGAAGAATTGAGCTCTTGTACCAATTAAATTCTTCGTAGTT
 AGATCAGCTAACTAGCTTAAAGAGATTCTTGGGTTATTGGTCAAATGT
 40 AGTGAATATTTACTGCTGTTCCCTCTCATTATAGGGTTACTATCCCTAAAG
 CCAAGTTACGGAAATATAAAAGCGTTATATTACTGCTTCTGATGTCTC
 TTTCATAGAGTGTACTCAAGTTAGATATTAAATAGATGCTAATCG
 GGTTTGAAATCGACGATCTATGGACAAATACCTAGGCGGTCTTCGC
 CCTATGGAGTTATCGAAACATAAAAGGTTGGCTTAACATTAGAAAATG
 A

MLKRLFTEDGELETKISRRFVWMLVVIYCLIIVRMCFGQIMIEGVSTPNVQRFG
 RIVALLVPFNSFRSLDQLTSFKEILWVIGQNVVNILLFPLIIGLLSLKPSLRKYK
 SVILLAFLMSLFIECTQVVLIDILANRVEIDDLWTNTLGGPFALWSYRNIKG
 WLLTIRK*

5

Sequence description:

10 A] Length: 516 bp - 172 aa (full-length gene)
 B] ATG start codon is preceded by an Shine-Dalgarno sequence. Possesses a potential leader peptide sequence. C-terminus need further confirmation.

15

ID-118

20

Clone 3-3

25 ATGAAAAAGCTTACTTTATTGGGATTAGATGGGACATTAATAGATTG
 TATGTACCAATTATGGAAGCTCTTGAAGAACCTATCGTCATTTGGCTTA
 ATATTGATAAAGAATTAATCCATGAATATATTTACAGGAATCAGTGGGG
 CAATTATTGGTAAACCTTTCAGAGGAAGAGCAAATACCTCATGAAAAACT
 GAAAGCATATTTACAAAAGAACAAAGAAAGTCGAGATTCTAAAATACATT
 TAATGCCATAATGCAAAAGAGATTAGAATGGACCAAGAACAGATATT
 CCCAATTTATGTATACACATAAAGGAGCAAGTACGCATTCACTGTTGGAA
 30 ACCTTGCAGATCTCTCATTATTTGATGAAATTTAATCTGGTGTTCGGGAT
 TCGAGCGAAAACCACATCCACAAGGGATTAATTATTTAGTTAACGATATT
 CTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTGG
 AGGTTGCTAAAATGCTGGTATAAAATCCATAAACTTAAGGTTAGAGAATT
 CCAAAGAAAATATAATATTCAAGTCTCAAAGATATAATACACTTGATT
 TCACTCGTTGGATTAA

35

MKKLTFIWLDLDTLIDSYVPIMEALEETYRHFGLIFDKELIHEYILQESVGQLL
 VNLSEEEQIPHEKLKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTH
 KGASTHSVLETQISHYFDEILTGVSGFERKPHPQGINYLVKRYSLDKSMTYI
 GDRPLDLEVAQNAGIKSINLRENSKENYNISSLKDIISLDFTRLD*

40

Sequence description:

A] Length: 627 bp - 209 aa (Possible Full-length gene)

B] ATG start codon is preceded by an possible Shine-Dalgarno sequence. No obvious leader peptide sequence.

5

ID-119

10
10

Clone 3-7

ATGGAAAAAGAAAAAAAATTAGGTCTTTACCACTAACAAATGCTTGTCAATTGGCTCTTTATCGGTGGCGGAATCTTGATTAAATGCAAAATATGAGTTCCAGAGCCGGTTGGTACCAATGCTTATTGCTTGGTAATTACTGCTATCGGGATGGGAACCTTCGTTTAAGTTCAAAATTATCTGAAAAAGGCCGGACCTAACAGCTGGAATCTTAGTTACGCTAAAGAGGGGTTGGAAACTTATGGGATTAAACTCTGCATGGGTTATTGGTTATCAGCTTGGCTTGGAAATGTTGCCTACGCTGCACTCTTATTCACTCGGTTATTCTTAAATTCTTGTGAATGGAAATAATATCATCTCAATTATTGGAGCAAGTATAAGTTATTGGGTTGTCCATTCTTAATTAAAGAGGTGTTAACAGCTGCATTATTAAACCGTAGTTACCTTGCACGTTACCTGTTATTATTCTTAATTTCAGCGTTATTAGCTTCAAATTAAACATTAGTTAGTCTGATATCTGGGAAATGGATTACATCAATCAATTTCACCAAGTCAATTCAACTATGAAAACCGCTGTTGGGTATTATTGGTATTGAGGGCGCCGTTGCTTCTCAGGTCGTGCTAAAAACACTCTGATATTGGTAAAGCAAGTATCCTAGCATTATTCACTATGATTCACTTATGTATTGATTCTGTTTATCACTGGTATCATGTCACGTCAGAATTGGCAACTAACCCAGCTATGGCTTACGTTAGAAAAAGCTGTTGGTCACTGGGGTGCATCTTAGTTAACCTGGTGTATCATTCACTATTGGCCTATTCTGCTTGGACTTATTGCAGCAGAATTACCATATCAAGCTGCTAAAGAAGGTGCTTCTAAATTGGCAAAAGAAAATAACAAAGCTCCAATCAACTCACTCTAGTCATACTTTGTGTACAAGCATTCTTAATCACGTTCTTATTCACACAAAGTGCCTATCGTTTGGTTTCGCATTAGCATCATCTGCTATCTTAATTCTTATGCTTTACAGCACTATATCAATTACAATTCAACCTCCGTGAGGATAAGTCAACTCCAGGACATAAAAGAATTAAATTACGGTATCCTCGCTACAATCTATGCTTACCTTATCTACGCTGGGGTTTGATTACTTACTTTGACAATGATTGCTTATACTCTAGGTATGATTCTATATTAAAATGAGAAAAGATGACAAGCTTGGCGTAATCATGGTCATAGCTGTTCCAGTGTGAAATTGTTATCC

MEKEKKLGLLPLTMLVIGSLIGGIIFDLMQNMSSRAGLVPMLIAWVITAIGMGTFVLSFQNLSEKRPDLTAGIFSYAKEGFGNFMGFNSAWGYWLSAWLGNVAYAALLFSSLGYFFKFFGNGNNIISIIGASIVIWVVFILRGVNTAAFINTVVTFAKLVPVIIFLISALLAFKFNIFSLDIWGNGLHQSFNQVNSTMKTAVVFIGIEAV

VFSGRAKKHS DIGKASILALFTMISLYVLISVLSLGIMSRPELANLKTPAMAYV
 LEKAVGHW GAILVNLGVII SVFGAILAWTLFAAELPYQAAKEGAFPKFFAKEN
 KNKAPINSLLVTNLCVQAFLITFLFTQSAYRFGFALASSA ILYAFTALYQLQF
 TLREDKSTPGHQKNLII GILATIYAVYLIYAGGF DYL LTMIA YTLGMILYIKMR
 5 KDDKLGVIMVIAVSSVKLLS

10 Sequence description:
 A] Length: 1356 bp - 452 aa (partial sequence)
 B] ATG start codon is preceded by an possible
 Shine-Dalgarno sequence. Possesses a potential
 leader peptide sequence.
 15

ID-120
 20 Clone 3-8

25 ATGAAATTGAAAAACGGCAGGTCTATTATGTTGT CATAACATTGCTATT
 TGCTATGCTATACAGGCTTATTGGGGAGCTGTTCTAATATTTAACTACGC
 TTCATAAGGCAATATTCCTTTGATGGAGCTGGAATTGCCTATATTAT
 TAATATTGTAATGTCAGTCTATGAGCGATTATATATAAAGCTTTAAAGG
 ATCTAGACTATTAATGGCAATCAAGCGTAGTGTCTATGATTTATCCTAT
 GCAACTTTATTGGTTAATTGTCTGGCTATTTCAATTGTATTCCAGATT
 30 TGATTCTAGTTGAGTTCTTATTGGTTATTGATAACGGAGCACTGCTAA
 ATTGGTTAATAATCTCAATGAAAATAACAAATTCTGAGGCCTTAAATTA
 TATGGGAACAGATAAAAGACTTAGTTCTACTTTAACGTTATAGCCAGCA
 GATTTGAAGCAAGTTTATCTGTTAACAAATTACTAACCTCAGTTCC
 TCTATTGCGGCAACACTTCTGAATGTTTTGTTAGTTATTGTTCAATT
 35 CGTTTGGCAAACAAGGAGCAGTTGGGACGTCAATTAAATTGTTAATTGA
 TACCTATTAGGTCAACAGGCAAACATTCCATTACGTTCGTCATATCCTT
 CATCAACGTTCCATGGTTTTGTAAGCCAAACTTAGAAGCTATGATT
 TAGGAAGTTGACGGTTATTGGTATGTTGATCTTCCAATTCCATTGCTT
 AACAGTTGGGTTTAGTTGCTTTACAGCTCTAACCGGTTGTGGGAGC
 40 CTACATTGGTGTACAATCGGTTCATCTTAATTGCTACTGAATCGCTTACT
 GAAGCATTCTGTTGTTCTTCTTGATCCTTTACAACAAATTGAGGGAA
 ATGTCATTATCCGAAAGTTGTCGGGATCGATTGGACTGCCTCTATGT
 GGGTTTAATGGCTATTACTATCGGAGGTGCTTATGGGGATCTTAGGCA

TGTTACTTGCTGTCCTGTTGCAGCTACTATCTATCAGATTGAAAGATCA
 TATTATCAAGCGACAAACGCTTAGAAATCGCACGAACCTATCGTTAA
 5 MKFEKRQVYYVVITFAICYAIQAYWGAVSNILTLHKAIFPFLMGAGIAYIINI
 VMSVYERLYIKLFKGSRLLMAIKRSVSMILSYATFIGLIVWLFSIVPDLISSLSS
 LLVIDTGALAKLVNNLNENKQISEALNYMGTDKDVLVSTLSGYSQQILKQVLSV
 LTNLLTSVSSIAATLLNVFVSFISIYVLANKEQLGRQFNLLIDTYLGSTGKTFH
 10 YVRHILHQRFHGFFVSQTLTEAMILGSLTVIGMLIFQFPYALTVGVLVAFTALIP
 VVGAYIGVTIGFILIAATESLTEAFLVFLILLQQFEGNVIYPKVVGGSIGLPSM
 WVLMAITIGGALWGILGMLLAVPVAATIYQIVKDHIKRQTLRNARTYR*

Sequence description:

15 A] Length: 1134 bp - 378 aa (full-length gene)
 B] ATG start codon is preceded by an typical
 Shine-Dalgarno sequence. Possesses a potential
 leader peptide sequence.

20

ID-121

25 Identical to ID-68, as described in WO 00/06736

ID-122

30 Clone 3-16

35 GTGATTACAATTAAAAAGGAATCTGTTATCAAACATTGAAGTATGCTTT
 GGCATTATAATGGGATTATTATCTTAGCTATTGTAATAGGTGGGCTCTA
 TTTGCATACTACGTTAGTCGTTCTCCGAAATTAAACCGATCAAGCTTAAAA
 TCCGTTAACTCTAGTTGGTTATGATGGTAATAATAAACTTATTGCCGATT
 TAGGCTCAGAAAAGCGTGAAGTGTAGTGCAGGATAGCATTCCACTAAAT
 40 TTGGTTAACGCTATCACTTCTATAGAAGATAAACGTTCTTAAACATAGA
 GGTGTCGATATTATCGTATTTAGGTGCAGCTTGGCATAACCTTGTAGTA
 GTAATACGCAAGGTGGTTCAACCCTGATCAACAGTTGATTAACACTGGCTT
 ACTTTCTACCAATAATCTGACCAACGTTAAACGTAATCACAGGAA
 GTTTGGCTTGCCTCAAATGGAGCGTAAATACACCAAAGAAGAAATTCTT
 ACTTTCTATATTAATAAGTTATATGGAAATGGAAATTATGGTATGAGA

5 ACAACAGCTAAATCATACTTGGTAAAGACCTAAAGGAATTATCTATTGCA
 CAACTTGCCTTGCTCGCTGGTATTCCCTCAAGCACCTACACAATATGACCCTT
 ATAAAAAACCCAGAATCTGCTCAAACAAGACGTAATACCGTTCTCAGCAG
 ATGTATCAAGATAAAAACATTCTAAAAAGGAATACGACCAAGCTGTTGC
 10 AACTCCAGTAACTGATGGCTTAAAAGAATTAAAGCAAAATCTACTTATCC
 AAAATATATGGATAACTACTTAAAACAAGTTATTAGTGAAGTTAACAAA
 AACTGGTAAAGATATCTTACTGCTGGCTAAAAGTGTACTAATATCA
 AACTGATGCACAAAACAACATATGACATCTACAAACAGTGATACTTAC
 ATCGCTTATCCAACAAATGAATTACAAATAGCATCTACCATCATGGATGCG
 ACTAATGGTAAAGTCATTGCACAATTAGGCGGGCGTCATCAGAATGAAA
 TATTTCATTGGGACAAATCAATCTGTCTTAACAGACCGCGATTGGGGTTC
 TACAATGAAACCTATCTCAGCTTATGCACCTGCTATTGATAGTGGTGTCTA
 15 TAATTCAACAGGTCAATCATTAACGACTCAGTTACTACTGGCCTGGTAC
 TTCTACTCAACTATATGACTGGGATCGTCAATATATGGGTTGGATGAGTAT
 GCAGACCGCTATTCAACAATCACGTAACGTCCCTGCTGTCAGAGCACTTGA
 AGCCGCTGGATTAGACGAAGCAAAATCTTCCTGAAAAATTAGGCATAT
 ACTATCCAGAAATG

20 MITIKKESVIKLKYAFGIIMGFIILAIVIGGLFAYYVSRSPLTDQALKSVNSS
 LVYDGNNKLIADLGSEKRESVSADSIPLNLVNAITSIEDKRFFKHRGVDIYRILG
 AAWHNLVSSNTQGGSTLDQQLIKLAYFSTNKSDQTLKRKSQEVLALQMER
 KYTKEEILTFYINKVYMGNGNYGMRTTAKSYFGKDLKELSIAQLALLAGIPQA
 PTQYDPYKNPESAQTRRNTVLQQMYQDKNISKKEYDQAVATPVTDGLKELK
 25 QKSTYPKYMNDYLKQVISEVKQKTGKDIFTAGLKVTNINTDAQKQLYDIYN
 SDTYIAYPNNELQIASTIMDATNGKVIQLGGRHQHENISFGTNQSVLTDRDW
 GSTMKPISAYAPAIDSGVYNSTGQSLNDSVYYWPGTSTQLYDWDRQYMGWM
 SMQTAIQQSRNVPNAVRALEAAGLDEAKSFLEKLGIYYPEM

30 Sequence description:

35 A] Length: 1386 bp - 462 aa (partial sequence)
 B] GTG start codon is preceded by an
 typical Shine-Dalgarno sequence. Possesses a
 potential leader peptide sequence.

40 ID-123

Clone 3-17

ATGGCTAATGTATGATTTAGCAAATGAATTAGAACGTGCTGTCGTGCT
 TTACCAAGAACAGCAGTTAACTGCAAAAGCAGCTATTGAAAATGA
 5 TCGGGATGCACAAGTGCCTTGGCAAGACTTTGGCTACCCAATCAAAAGT
 TCAAGAAATGATGCAATCTGGCAAATGCCAAGTCAAGAAGAACAAAGATG
 AAATGTCTAAACTTGGGGAAAAAATTGAATCCAATGACCTTTAAAAGTTT
 ATTTGACCAACAAACACGGTTGTCTGTATATGTCTGATATCGAAAAAAA
 TTGTCTTGCACCCATGCAGGACTTGATGTAA

10 MANVYDLANELERAVRALPEYQAVLTAKAAIENDADAQVLWQDFLATQSK
 VQEMMQSGQMPSQEEQDEMVKLGEKIESNDLLKVYFDQQQRLSVYMSDIEKI
 VFAPMQDLM*

15 Sequence description:
 15 A] Length: 336 bp - 112 aa (full length sequence)
 B] ATG start codon is preceded by an
 typical Shine-Dalgarno sequence. No obvious
 potential leader peptide sequence.

20

ID-124
 25 Clone 3-26

30 ATGGCAGAAATCACAGCTAAACTTGTAAAAGAATTGCGTGAAAATCAGG
 TGCAGGGCGTTATGGACCGCTAAAAAAGCATTAGTAGAAACTGATGGTGACC
 TTGATAAAGCGATTGAATTACTTCGCGAAAAAGGTATGGCTAAAGCAGCT
 AAAAAAAGCAGACCGTGTGCTGAAGGTTAACAGGTGTTATGTTGAT
 GGTAACGTTGCAGCAGTTATTGAAGTTAA

35 MAEITAKLVKELREKSGAGVMDAKKALVETDGDLDAKIELLREKGMAKAAK
 KADRVAAEGLTVYVDGNVAAVIEV

40 Sequence description:
 40 A] Length: 230 bp - 76 aa (partial sequence)
 B] ATG start codon is preceded by an
 typical Shine-Dalgarno sequence. No obvious
 potential leader peptide sequence.

5 ID-125

Clone 3-33

10 ATGATAAAAAACCTGTTATTAACAGGTTTTATCATTAAATGACGGAAAA
CTGGACACAAATTATTTCTGTATAATTAAATATTATTCAGG
AGGTTATGATGACATTAGAGAAACGATTAA

15 MIKNLLLTGFLSFNDKLDNYFSCIKYIISYQEVMMTLEKRF

Sequence description:

20 A] Length: 134 bp - 44 aa (partial sequence)
B] ATG start codon is preceded by an
typical Shine-Dalgarno sequence. Possible
potential leader peptide sequence.

25 ID-126

Clone 3-41

30 ATGAAAAATAATAAAAATAATGGTTTCTGAAAAATTCTTTATTACATA
TTATTGATTATTGCGGTTATTACAACCTTCAAACTATTAA

35 MKNNKNNGFLKNSFIYILLIAVITTFQYYL

Sequence description:

40 A] Length: 94 bp - 31 aa (partial sequence)
B] ATG start codon is preceded by a
possible Shine-Dalgarno sequence. Potential
leader peptide sequence.

ID-127

5

Clone 3-42

10 ATGTTAGATATTATCTTATCCGAATTCGCAAGGATTACTTGGTCAATTATGGCAATTGGCGTGTTCACTTTCGTATCTTAGACATAGCCGATCTCTCTGCAGAAGGGCTTCCCTATGGGGCTGCAGTTGCGCCTATGTATCGTTAA

15 MLDIILSGISQGLLWSIMAIGVFITFRILDIADLSAEGAFPMGAACVACLCIV

Sequence description:

20 A] Length: 158 bp - 52 aa (partial sequence)
B] ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential leader peptide sequence.

25

ID-128

30 Clone 3-43

35 ATGGAAATGCCTAAAAGAAATGAATTACTCAATAAAGAAATTAAAATGAGTATTGATAAACTTAGATATAAAGAACCAAGAGAGTGAACATGACAAGCGACTACTTTTATTGGTAGTACTTATACTGTTACTGTAGCAGTTATATTGTCGTTATTTAA

MEMPKRNELLNKEIKMSIDKLRYKEPESEHDKRPTFYLVVLILVTVAVILSLF

40 Sequence description:

A] Length: 161 bp - 53 aa (full-length gene)
B] ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential

leader peptide sequence.

ID-129

5

Clone 3-44

10 GTGGTAAGTAAATTGAGTTAACAAACGATTTCGCATTGCTATTTCATCA
ATGCTAATTACGCAACACCTCTTACAGTATTGGGGAACCTTC
TCTGAACGTGGTGGTATCGTCAACGTTGGTTAGAAGGAATTATGGTAATT
GGAGCTTCTCAGGCAGTGTATTAA

15 MVSKLSLTTIFALLFSSMLIYATPLIFTSIGGTFSERGGIVNVGLEGIMVIGAFSG
VVF

20 Sequence description:

25 A] Length: 179 bp - 59 aa (partial sequence)
B] GTG start codon is preceded by a
possible Shine-Dalgarno sequence. Potential
leader peptide sequence.

ID-130

30

Clone 3-46/47

35 ATGAGAATTATTGCAATAACTGAAAAGGTTATAAAAGAACTGTTCGTGAT
AAAAGAACACTTGCTATGATGTTTCTGCACCTATTAAATTATGTTTGA
TGAATGTTATGTTTCTGCAGATAGTAATACAAAAGTTAAGATTGGAACCA
TTAACGTTAACACGAAGGTGTTCAAATTAGATAATATTAAAGCATATT
AAGTGAGATCATTAAATTAACTCATCTGCTAAAAAGCACTCAAATCAA
ATAAAATTGATGCTTATTGAGGACAATAATCTTACTGTCTTCT
40 ATGCGAACATACAGATTCTCAAAGACGGACTTAACAAGACAAAGCTTTAAA
ACCGCTGTTAACATGAAACAGTAAGGAACGTGATTGCAAGTTAAATT
TTAGCTAATAAGAACATCGAAACTAGCACAATCCTACAAACTCGCTCCAAA
TATATCAAAGAAAAATAATTACGGAAATAAAAATACAGGGCTTTTGC
AAAAATGATACCAATACTAATGGGATTATGGTCTTCTGGTTTT

5 MRIIAITEKVIKELFRDKRTLAMMFLAPILIMFLMNVMFSANSNTKVKIGTINV
NTKVVSNLDNIKHIQVRSFKFNSSAKKALKSNKIDALISEDNKSYTVFYANTDS
SKTTLTRQAFKTAVNTMNSKELISQVKILANKNPKLAQSLQTRSKEYIKEKYN
GNKNTGFFAKMIPILMGFMVFFLVF

5

Sequence description:

10 A] Length: 558 bp - 186 aa (partial sequence)
B] ATG start codon is preceded by a possible Shine-Dalgarno sequence. Potential leader peptide sequence. C-terminus has yet to be determined.

15

ID-131

20

25 GTGATTATCGTTATGAGTAAACATCAAGAAATTTGGAGTACCTAGAAAAT
TTAGCTGTTGTAAGAGGGTTAGTGTACGCAGTATTCAAATCATTAA

MIIVMSKHOEILEYLENLAVGKRVSVRSISNHL

30 Sequence description:

35 A] Length: 100 bp - 33 aa (partial sequence)
B] GTG start codon is not preceded by a
obvious Shine-Dalgarno sequence. No obvious
leader peptide sequence.

ID-132

40

Clone 2-c53

ATGTATAGAGAAATTACCGCTGTCAACACGATCGCTTGTGAGCGAATCC
 AACCAAACAAACCTACTTCAATCTCTTAATTGGCCCAAAGTAAAAGACAA
 CTGGGGTAGTCAATTACTTGGCTTTTGACGGTAAACCCAAATTGCCAG
 5 CGCTAGTATTCTCATCAAATCACTCCCTCTGGCTTCCATGCTGTATATT
 CCGCGTGGACCAATCATGGATTACTCCAATCTAGATATTGTAACTAAGGTC
 CTTAAGGACCTTAAAGCTTTGGCAAAAAACAAAGAGCTCTTTATCAAG
 TGTGATCCTCTCATCTATT

10 MYREITAVEHDRFVSESNQTNLLQSLNWPKVKDWNWSQLLGFDFGETQIASA
 SILIKSLPLGFMSMLYIPRGPIMDYSNLDIVTKVLKDLKAFGKKQRALFIKCDPLI
 Y

15 Sequence description:

20 A] Length: 326 bp - 108 aa (partial sequence)
 B] ATG start codon is preceded by an obvious
 Shine-Dalgarno sequence. No obvious leader
 peptide sequence.

25 ID-133

Clone 2-c59

30 ATGGACAAGAAAAAAATCTTAGTAACGGGTATTGTGCCTAAAGAAGGTCT
 AAGAAAGCTTATGGACCGATTGATGTTACTTATTCAAAGATGCCATT
 TTCACGTGACTATGTGTTAGAGCATTATCTGAATATGACGGATGGTTACT
 35 CATGGGACAAAAGGTGATAAAGAGATGATTGATGCAGGTGAAAACCTAC
 AAATTATTTCTT

MDKKKILVTGIVPKEGLRKLMDRFDVTYSEDRPFSRDYVLEHLSEYDGWLLM
 GQKGDKEMIDAGENLQIIS

40 Sequence description:

A] Length: 215 bp - 71 aa (partial sequence)

B] ATG start codon is preceded by an obvious Shine-Dalgarno sequence. No obvious leader peptide sequence.

5

ID-134

10 Clone 2-c62

15 ATTCGAAAGATGACTACCAAAATATTAGTTTGGACAGGATCCAGAAGTT
 GTTGATTATGCTGGTCTGTTGAAAAACGCCGTCCAGTTAGAAAAAGCA
 GTTAAAAATTCTTGCAGAAAGAGAGAGCTACGAGAATGCTATCTGATTTC
 TTGCAAGAAGAAAAATGGGTAACTGATTTGCTGAATTATGGCGATCAA
 AGAACATTGGTAATAAGGGCCTCAAGAATGGGATGACAAGGCTATT
 TACGCCGCGAAGAAGAACGCCTAGCAGGATATCGTCAAAAGCTTAGTGAA
 20 GTGATAAAATATCATGAAGTAACGCAATATTCTTTACAAACAATGGTTT
 GAGTTAAAAGAATATGCTAATGATAAAGGGATTCAAATTATCGGTGATAT
 GCCAATCTACGTTCTGCCGATAGTAGAAGTTGGACAATGCCTGA
 25 GTT
 ISKDDYQNISFGQDPEVVVDYAGLFEKRRPVLEKAVKNFLQEERA
 EEKWVTDFAEFMAIKEHFGNKALQEWDKAIIRREEALAGYRQKLSEVIKY
 HEVTQYFFYKQWFELKEYANDKGIIQGDMPIYVSADSVEVWTMPELF

30 A] Length: 459 bp - 153 aa (partial sequence)
 B] More sequencing is required to determine the
 N- and C-termini
 enzyme). - *Streptococcus pneumoniae* (63%)

ID-135

35 Identical to ID-108 described in WO 00/06736

40 Clone 2-c63

ID-136

Clone 2-c66

5 ATGGCAAAACAGAAAAATAACTGGCGCCGTGTTGGAGTTGGTGTCTTAC
 ACTTGCTTCAGTTGCGACTCTGCTGCATGTGGAAGTAAATCAGCTCCCA
 GGATTCTAATGGAGCGATTAAATTGGGCTATTCCAACAGAAATCAATACACT
 AGATTATCTAAAGTTACAGACACTTACTCAAATCTAGCTATTGGTAACCTC
 TAGTAGTAATTTCCTTCGCTTAGATAAAAGATGGAAAGACAAGACCCAGACTT
 10 GGCTACTAAAGTTGATGTTCAAAAGATGGCTTAACCTATACAGCTACATT
 ACGTAAAGGCTTGAAGTGGTCAGATGGCAGTAAACTTACTGCAAAGGATT
 TTGTTTATTCATGGCAACGTTAGTTGATCCTAAAACAGCTTCACAATATG
 CTTACCTTGCTGTTGAAGGGCATGTGCTTAATGCCATAAAATCAACGAAG
 GACAAGAGAAAGACTTGAATAAGCTAGGTGTTAAGGCAGAAGGCGATGA
 CAAAGTTGTTATTACTTATCTAGTCCGTCTCCGCAATTCTACTACCTT
 15 GCATTCACTAACTTCATGCCACAAAAACAAGAAGTTGTTAAAAATATGG
 AAAAGATTACGCAACTACTTCAAAAAATACAGTTACTCAGGACCATATA
 CTGTTGAAGGTTGGAATGGTTCGAATGGTACTTCACGCTGAAGAAAAAC
 AAAAATTATTGGGACGCTAAAATGTAAAACAAAAGAAGTTCGCATCCA
 GACTGTTAAAAAACCAGATACCGCCGTTCAAATGTATAAACGTGGTGGAGT
 TAGATGCAGCTAATATCTCAAATACTTCTGCTATTATCAAGCTAATAAAAA
 20 ATAATAAAAGATGTACAGATGTTCTAGAAGCGACCACTGCCTATATGGAA
 TATAATACTACTGGTTCTGTGAAAGGGCTTGATAATGTTAAGATTGTCGC
 GCCTTAAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGAT
 ACAGGCTCAAAACCGGCAATTGCTTGCACCTACTGGTTAGCCAAAACA
 CCAGATGGAACTGATTGGCAAAATATGTTGCCAGGTTATGAATATAAT
 25 AAAACTGAAGCAGAAAACCTTTAGACTA

 30 MAKQKNNWRRVGVLTLASVATLAACGSKSASQDSNGAINWAIPEINTLD
 LSKVTDTSNLAIGNSSSNFLRLDKDGKTRPDLATKVDVSKDGLTYATLRKG
 LKWDGSKLTAKDFVYSWQRLVDPKTASQYAYLAVEGHVLNADKINEQKEK
 DLNLGVKAEGDDKVITLSSPSPQFIIYLAFTNFMPQKQEVVEKYGKDYAT
 TSKNTVYSGPYTVEGWNGSNGTFTLKKKNYWDAKNVKTKEVRIQTVKKPD
 TAVQMYKRGELDAANISNTSAIYQANKNNKDVTDVLEATTAYMEYNTTGSV
 KGLDNVKIRRALNLATNRKGVVQAAVDTGSKPAIAFAPTGLAKTPDGTDLAK
 YVAPGYEYNKTEAAKLFR

35

Sequence description:

40

A] Length: 1143 bp - 381 aa (partial sequence)
 B] Shine-Dalgarno sequence precedes ATG codon.
 Possesses a potential leader peptide sequence.

ID-137

Clone 2-c67

5

TTGAGAGTTATGAAAATAAGAAGAGTTGAAAAAAGAAATAAGTAAAAC
 ATTGAGAAATACATTATGGAATTAAATAA
 10 TATTCCAGAGAATCTAAAAGATAAAAGAATTGATGAAGTTGATAGAACTC
 CAGCAGAAAACCTTCTTATCAGGTTGGCT
 GGACCAACTTGGTTCTTAAATGGGAAGAAGATGAAAGAAAGGGACTCAA
 GTAAAAAACACCATCGGATAAATT
 15 MRVYENKEELKKEISKTFEKYIMEFNNIPENLKDKRIDEVDRTPAENLSYQVG
 WTNLVLKWEEDERKGLQVKTPSDKF

Sequence description

20

A] Length: 234 bp - 78 aa (partial sequence)
 B] TTG start codon is preceded by a
 potential Shine-Dalgarno sequence. No obvious
 leader peptide sequence.

25

ID-138

Clone 2-c70

ATGTCAAAGTTGATAGTCAGAAAATAATTACTCCGATTATGAAGTTGTC
 AATATGCGAGGGATTATTGCACTCAAAGATGGCATGCTAGCAATTTCACCA
 35 CTAACAGTTGGAGTCTCTTTAATATTAGGCAGCTTCCATT
 MSKFDSQKIIPTIMKFVNMRGIIALKDGMALILPLTVVGSLFLILGQLPF

40 Sequence description

A] Length: 150 bp - 50 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 Shine-Dalgarno sequence. Possesses a potential

leader peptide sequence.

ID-139

5

Clone 2-c71

10 GAGACCACCTCATCAGTTAAACCAGCAGGAATTGACCGTATCAATCATACC
 TCAACACCCCCGAAGAAAACTACCCCCAACATTGCAACGACGCATAGCTT
 CAAAGATCGTGTGATACTTTAGAAAGAATTACAATGAAGACATTGATGT
 TTGTTCTGGATTCAATTGTGGTATGGGAGAGAGCGATGAGGGGCTCATCAC
 15 ATTAGCTTCAGACTAAAAGAACTGAACCCCTATTCTATCCCTGTCAATT
 TTACTTGCTGTTGAAGGAACACCTCTGGAAAATATAACTATTTGACTCCC
 ATTAATGCTAAAAATTATGCCATGTTGCGTTTGTTCCTTCAAGG
 AATTAAGATTAAGTGGACGGGAGGTCCATTGAGAAATTGAATCAT
 TAGTCACCTTACTTGTGACTCAACTTTTGGAAATTACCTAACAGAGG
 20 GGGTCGCAATCAACATACCGATATTGAATTCTGGAAAAATTACAAC
 AATCATACTAAAAAGGAATTAATT
 ETTSSVKPAGIDRINHTSTPPKKTPNIAUTHSFKDRCDTLERIHNE
 25 DIDSVCVSGFI
 CGMGESDEGLITLAFLRKELNPYSIPVNFLAVEGTPLGKYN
 LTPIKCLKIMA
 MLRFVFPFKELRLSAGREVHFENFESLVTLVDSTFLGN
 LTEGGRNQHTDIEF
 LEKLQLNHTKKELI

Sequence description:

30

- A] Length: 535 bp - 178 aa (partial sequence)
- B] N- and C-termini require verification

35

ID-140

40

Clone 2-c73

ATGCCGGTTGGACTGCACAGTCTATTCAAAGGCATTTAGAAAAGCAT
 AATACTAAGGAAGGCACCTGGGAAAACCTAACCAATTCTAAGTGGTTCTTA
 GTATTTACCAAGTTATCTCCTGATGGAGAGGAAATCTCGCGGCATATTTT

GATGCTAGTAGTGTATTCCCTTTGTTGATCCACAAAGTCTGGCATAAAGTT
 TCGCCGAATAGTCCAGACTTAAGTTGCTATCTAACCTTTACTGCCAAAAAA
 GAAGATTACTCCATAAAAATATGGTCTCACGCGCACACATTCTGAGGTT
 5 ATCGCCAGTGCACCTCTCTTATCTGAGAAGAGTAATATATTAGACCTTGGG
 TGTGGTCAAGGGCGAAACTCACTTATTATCGCTGCTGGGACATCAAGTG
 ACTTCTGTCGATTCAAACGGACAGAGCCTGTAGCTTAGAAAATATGGCA
 TTAGAAGAAGAGCTTCCTTACAATATAAAAAGGTATGATATTAACTACT
 GCTATTGAAGGGCACTATGATTTATTTACTCAACTGTGGTATTATGTTTT
 T
 10 MPVWTAQSIPIKAFLEKHNTKEGTWAKLTIISGSLVFYQLSPDGEIISRHIFDAS
 SDIPFVDPQVWHKVSPNSPDLSCLTYCQKEDYFHKKYGLTRHSEVIASAP
 LLSEKSNILDLCGQGRNSLYLSLLGHQVTSVDSNGQLVALENMALEEELPY
 15 NIKRYDINTTAIEGHYDFILSTVVFMF

Sequence description:

20 A] Length: 563 bp - 187 aa (partial sequence)
 B] N- and C-termini require verification

25 ID-141

Clone 2c76

30 ATGACAAAGCAAATAATTGCCATTGGGGCTGAAGATGAAGACCATTGAT
 TGGAGTTAATGGCGGTTACCATGGAGGCTCCTAAAGAGTTACATCACTT
 CAAAGAAACGACCATGGGGCAGGCTTGCTTATGGGACGAAAGACCTTTG
 35 ATGGAATGAACCGTCGTACCTGGTAGAGAGACAATCATCTTAACAA
 AAGATGAACAATTCCAAGCAGATGGAGTGACAGTCCTAAATAGTGTGAA
 CAAGTTATAAAATGGTTTCAGGAACATAATAAGACCTTATTATTGTAGGT
 GGTGCAAGTATTATAAGCATTCTGCCTTATTGTGAAGCAATCATAAAA
 ACTAAAGTTCATGGAAAATTCAAAGGTGATACCTATTTCCGTATGTTAAT
 CTATCTGAGTT
 40 MTKQIIAIWAEDEDHLIGVNGGLPWRLPKELHHFKETTMGQALLMGRKTFDG
 MNRRVLPGREIILTKDEQFQADGVTVLNSVEQVIWFQEHNKTLFIVGGASI
 YKAFLPYCEAIIKTVHGKFKGDTYFPDVNLSEF

Sequence description:

5 A] Length: 417 bp - 139 aa (partial sequence)
 B] ATG start codon is preceded by a Shine-Dalgarno sequence. No leader peptide sequence

10 ID-142

Clone 2-c78

15 TTGTGGCCAAACTGTGCCCGCTTATTAATAGCACTTGTTCACCATTGAA
 GATATCTAACATCAGGTGCTCATAGCAACCTATTTAATGGGGTTATA
 CTTGGCGGGACAATTGTAGTAGTGGCGACAGCACCCTTCTTCTATGGCA
 TTGACAGCTATGCTAGGATTAACCGGAATGCCTATGGCTATAGGAGCCTTG
 TCTGTCTTGTTGTCGTCTTATGAATGGTGTACTTTCCATAAATTAAAAC
 TTGGAAGTCGTAAGATAATATAGCTTTGCTGTTGAGCCTCTAACTCAAG
 CTGACGTGACTTCAGCTAACCTATTCAATCTATGTCACTAATTGTTGG
 TGGTGCAGCTTGTGGTATTTAATTGCCTTGATGAAATTAGTTAATGATACT
 CCTGGAACAGCGACACCAATTGCAGGATTGCTGTATGTTGCCTATAAC
 CCAATGATAAAAGTACTAATAACCGCTCTAGGTTGTATTATCCTATCTTA
 CTAGCAGGCTATTGGAGGCATTGTTTT

 MWPNCAPLINSTLFTIEDILTSGAHSNPILMGVILGGTIVVVATAPLSSMALTA
 MLGLTGMPMAIGALSVFGSSFMNGVLFHKLKLSRKDNIAFAVEPLTQADVT
 SANPIPIYVTNFVGGAACGILIALMKLVNDTPGTATPIAGFAVMFAYNPMIKVL
 ITALGCIILSLLAGYFGGIVF

Sequence description:

35 A] Length: 540 bp - 180 aa (partial sequence)
 B] N- and C-termini have yet to be elucidated

40

ID-143

ID-145

5

Clone 3-86

10 ATGTCATATTTAGAAATTACTGGTATCGTTGGAGCAATTTATTATTA
 TTTAGCAGTAATATTGCTTGTAGACCTGACTGGTCAATGCTTCACTA
 TCTATTGTATTTACTTATGGCACTCTAGCGCATCAATTGAAGAATAT
 CAGTTCCCGGTGGGCATCACCTATCATTAACTATGTTGTTATGATGAA
 GAAGAGCTGATGGATTGTTCCAGGCAAACTCAGTCTATTATGTTGGTT
 AATACTATTGCTGGGTGCTTACATTGCTAGTATTGCTTCTCAAGCTT
 15 ATTGGCTTGGATTAGGAGTCATGTTCTTAGTCTAACGCAGCTTGGTC
 ATGGTTTCAGATGAATATTAAACTAAACTGGTATAATCCTGGTCTAG
 CAACGACAGTATTCTCCTAGTACCAATAGCTTGCACATCTATCAAG
 CTAGTGCAGAAGGAATGCTCACTGGGAGATTGGCTAGGTGGTTTATCA
 20 TGTTGATTGTCGTGACTAACTAGCATTATTGCACCTGTACAGCTATTGAA
 GGATAAGGAGACCAATTATATTAGTCCTGGCAAATGGACCCTTCA
 TAAGGTCGTTAATTGTAAGGATAAAAAAATAA
 MSYFRNYWYRFGAILFIILAVILLVFRPDWSMLHYLLYFYFMALLAHQFEEYQ
 25 FPGGASPIINYVVYDEEELMDCFPQNTQSIMLVNTIAWLLYIASIAFPQAYWLG
 LGVMFFSLTQLLGHGFQMNIKLKTWYNPGLATTVFLVPIACAYIYQASAEG
 MLTWGDWLGGFIMLIVCVLTSIIAPVQLLKDKETNYIISPWQMDRFHKVVNFV
 RIKK*

30

Sequence description:

35

A] Length: 651 bp - 219 aa (full length gene)
 B] Putative ATG start codon is preceded by a
 typical Shine-Dalgarno sequence. Possesses a
 potential leader peptide sequence.

40

ID-146

Clone 3-c88

Clone 2-c80

5 ATGTTTTAAGTATAATGGCAGGTGTCATAGCATTGCTCTGACAGTTATT
 GCCATTCCACCGCTTCATTAAGTTTACCAATTGAAGAAAATTGGCGGGCAA
 CAAATGCATGAAGATGTCAAACACATCTAGCCAAAGCAGGTACGCCGAC
 AATGGGAGGAACGGTATT

10 MFLSIMAGVIAFVLTVIAIPRFIKFYQLKKIGGQQMHEDVKQHLAKAGTPTMG
 GTVF

Sequence description:

15 A] Length: 172 bp - 57 aa (partial sequence)
 B] Shine Dalgarno sequence precedes 'ATG' start
 codon. Possesses a potential leader peptide
 sequence.

20

ID-144

25 Clone 3-83

30 ATGAAACCATATTATCTTTATTGGTAGAACGTTATTATACTTCGGTATT
 TATTGTTACTAATTACTTTTGCAACCTGGTCGGACAAGGCAGTT
 TATTTATAAA

MKPYLSFIGRTLLYFGILLLIYFFAYLGRGQGSFIY

35 Sequence description:

40 A] Length: 113 bp - 37 aa (partial sequence)
 B] Putative ATG start codon is preceded by a
 typical Shine-Dalgarno sequence. Possesses a
 potential leader peptide sequence.
 This orf is not in frame with nuc

ATGCCACTTACAGCACTGAAATTAAAGATAAAACATTTCATCAAAATT
CGCGGTTATAGCGAAGAAGAAGTT

5 MPLTALEIKDKTFSSKFRGYSEEEV

Sequence description:

10 A] Length: 75 bp - 25 aa (partial sequence)
B] Putative ATG start codon is preceded by a
typical Shine-Dalgarno sequence. No leader
peptide

15 ID-147

20 Clone 3-90

25 ATGTCACTTTCAAGAAAAATTGCTTACAATTGCGCTAAAAGGAAGCG
CTTTATAAAGAGAGTTAGGACGCTACGCCCTGAGATCAATGCTAGCAGG
GGCTTATTGACAATGAGTACTGCTGCCGGTATCGTCGCAGCTGATACTAT
TGGTAAAATTCTCCTGCTCTACAGGTTTGTATTGCTTCATCTTAGTT
TTGGACTTATTATGTTAATATTAAATGGTGAATTGGCGACATCTAATAT
GCTTATCTCACTGCAGGAGCCTATAATAAAAATCTCTGGAAAAAGC
30 CATAACAATTAAATTATTGTACTTTTCAACCTCGTTGGTGTATA
TTAGCTTGGTTGTTAA

35 MSLFQEKIAYNCACKEALYKESLGRYALRSMLAGAYLTMSTAAGIVAADTIG
KISPALSGFVFAFIFSGLIYVLIFNGELATSNMLYLTAGAYNKNISWKKAITILI
YCTFFNLVGACILAWLF

Sequence description

40 A] Length: 406 bp - 125 aa (partial sequence)
B] Putative ATG start codon is preceded by a
typical Shine-Dalgarno sequence. Possible
leader peptide

ID-148

5

Clone 3-92

10 AAGTTACAAGCGACTGAAGTTAAGAGCGTCCGGTAGCACAACCAGCTTC
 AACAAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCAACCTC
 ATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAA
 TTCAGTACATACCGTGCAGGAGATCCAGGTGATCATGGTAAAGGTTAGC
 AGTTGACTTTATTGTAGGTAAAACCAAGCACTTGGTAATGAAGTTGCACA
 GTACTCTACACAAAATGGCAGCAAATAACATTTCATATGTTATCTGGCA
 15 ACAAAAGTTTATTCAAATACAAATAGTATTATGGACCTGCTAATACTTG
 GAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCACGT
 TCACGTATCATTAA

20 KLQATEVKSVPVAQPASTTNAVAHPENAGLQPHVAAYKEKVASTYGVNEF
 STYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQ
 KFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSF

Sequence description

25

A] Length: 419 bp - 139 aa (partial sequence)
 B] N- and C-termini have yet to be determined

30

ID-149

35

Clone 3-94

40 ATGATTCCAGTAGTTATTGAACAAACAAGTCGTGGTAGACGTTCTATGAT
 ATTACTCACGTCTTTAAAAGATCGTATTATTATGTTGACAGGCCAAGTT
 GAGGATAATATGGCCAATAGTATCATTGCACAGTTATTGTTCTCGATGCA
 CAAGATAATACAAAGGATATTACCTTATGTCAATACACCCAGGTGGTTCA
 GTATCGGCTGGACTTGCTATTGTGGACACCATGAACTTCATTAAATCGGAC
 GTACAGACGATTGTTATGGGGATGGCTGCTCGATGGGAACCATTATTGCT
 TCAAGTGGTGCCTAAAGGAAAACGTTTATGTTACCGAATGCAGAATATG

5 ATCCACCAACCAATGGCGGAACAGGCAGGAGGTACACAGCAATCTGATAT
 GGCTATCGCTGCTGAGCATCTTTAAAAACCGTCATACTTAGAAAAAAAT
 CTTAGCTGATAATTCTGGTCAATCTATTGAAAAAGTCCATGATGATGCAGA
 10 GCGTGATCGTGGATGAGTGCCTAAGAACACTGATTATGGCTTATTGAT
 GCTATTATGGAAAATAATAATTACAATAATAGATTAAAAGAGTTGAGTT
 TACCAACTCTTTTATTGTTGAATTATGTTATAATCTTAGTAATTACA
 GATATGACGCAGAAAGGAAAAATTATTGA

10 MIPVVIQEQTSGERSYDIYSRLLKDRIIMLTGQVEDNMANSIIAQLLFLDAQDN
 TKDIYLYVNTPGSVSAGLAIVDTMFNIKSDVQTIVMGMAASMGTIASSGAK
 GKRFLMLPNAEYMIHQPMGGTGGGTQQSDMAIAAEHLLKTRHTLEKILADNSG
 QSIEKVHDDAERDRWMSAQEHLIMALLMLWKIIYNNRFKRVEFTNSFFICW
 NYVIILVITDMTQKGKNY*

15
 Sequence description

20 A] Length: 693 bp - 231 aa (full length gene)
 B] Putative ATG start codon is preceded by a
 typical Shine-Dalgarno sequence. No leader
 peptide. Significantly, it would appear to have a
 very hydrophobic C-terminus.

25 ID-150

30 Clone 2-c86

35 ATGAAACCAAAATATTGGTGTACTTGGCTAGGAATATTGGACAAACA
 CTCGCACAAGAACTAAGTAACCTTGAACAAAGATGTTATTGCTATTGACAGC
 AATCCTGAAATGTACAAGCTGTCGCCGAAGT
 TGTTACAAAGCAGCTATCGGAGACATTACTGATTAGCTTCCTAAAACA
 CATCGGGATCAGTGAATGTGATACTGTTATTATTGCTACAGGAAACAGTTT
 AGAGAGCTCAGTATTGGCCGTAAATGCACTGTAAAAACTTAGGCGTCCCAC
 AAGTTATTGCTAAAGCTGAAACCTGTATACGAAGAAGTACTTTATGAAA
 TTGGTGTGATTGGTTATCTCTCCGGAGCGAGAATCTGGCAAAATGTTG
 40 CTGCAAACCTCATGAGAAATAAAATTACAGATGTCTCCAGATTGAATCTG
 ATATTCTGTCAATTGAATT

MKPKIIGVLGLGIFGQTLAQELSNFEQDVIAIDSNPENVQAVAEVVTKAAIGDI
 TDLAFLKHIGISDCDTVIATGNSLE

SSVLAVMHCKKLGVQVIAKARNLVYEEVLYEIGADLVISPERESGQNVAAN
LMRNKITDVFQIESDISVIEF

5 Sequence description:

10 A] Length: 459 bp - 153 aa (partial sequence)
B] Putative ATG start codon is preceded by a
typical Shine-Dalgarno sequence. Possesses a
potential leader peptide sequence.
This orf is not in frame with nuc

15 ID-151

20 Clone 2-c88

25 GTGCCTTATAGTAAAGAGATTATCAGTTAGCTATACCAGCTATGATTGAA
AATATCTTACAAATGCTCATGGGAGTAGTTGATAATTATCTAGTGGCTCAG
TTAGGTGTTGAGCAGTATCAGGTGTTCAAGTAAATAATTACT
ATTATCAAGCTATTTTATAGCTTAGGGGGAGTATAGCAAGTCTATTG
GCCAAGTCGTTAGCAGGTAGTGAGAAGGATGATGCAATTCAAGTATGTTCT
CAAGCCATTCTAACATCACTGATAGGGCAGTATTAGGAATTATCTCG
ATTGTTTGGACAAACTTCTT

30 MRYSKEIIQLAIPAMIENILQMLMGVVVDNYLVAQLGVVAVSGVSVANNIITIY
QAIFLALGASIASLLAKSLAGSEKDDAISVCSQAIFLTSLIGAVLGIISIVFGQTFF

35 Sequence description

40 A] Length: 330 bp - 110 aa (partial sequence)
B] Putative GTG start codon is preceded by a
typical Shine-Dalgarno sequence. May have a
leader peptide

ID-152

Clone 2-c92

5 TTGATTAACAAGTATCGTCTTTGAAGAGGATTCTCCATAATAACT
 CCTTTAATAGTTATCGTGAGAAGTATTTAAAGAAAAACGCCAAGGTAG
 AGCGACATTTCTGCCTTAACATAAAACCAAGAGAATTAGCACAAC
 10 ATTATCTCTCAAAATTACAAAGTTCTCAAGGGTTTAGGAATAGCTAGTG
 AATTGGTAACTATGATCAACGCTTGTCAAACATT
 MINKYSCFLKRILHNNTPLIVIVRSILKKNRQGRATFLPLTTIKPRELAQHYLSK
 LQSSQGFLGIASELVTYDQRLSNIF

15 Sequence description

20 A] Length: 240 bp - 80 aa (partial sequence)
 B] No obvious Shine Dalgarno sequence precedes the Putative TTG start
 codon

ID-153

25

Clone 2-c94

30 TTGTTGACTCACAAAATATATTATTAACCATTATTTGGATTATTATGA
 TTATATTATCAGCATGTGGTATGTCTAATAAGGAAATGGCTGGTATTGATA
 ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAAT
 ACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTACTATACCGGCTTG
 ATATTGATTAGCTAATGCTTTAAAGAATACGGTATTCACTGAAAT
 35 GGCAGCCTATTAACTGGGATATGAAAGAAACTGAACCTAATAATGGTAAT
 ATAGACCTTATTGGAATGGTTATTCAAAACGGCAGAACGTGCTAAAAA
 AGTCGCTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAA
 AACTTCATCACATATTAAATAGTATTAAGGATATGAAGGGGGAAAAACTAG
 40 GAGCCCAGTCGGGTTCATCTGGTTTGATGCTTTAACGCTAAACCTGATA
 TTTAAAAAAAGTTGAAAAGGAAAAGAAGCAGTTCAATACGATACTTC
 ACTCAGGCTTGATTGATTAAAAAATAACCGTATTGATGGTCTTTGATT
 GATGAAGTTATGCTAACTATTAAAGCAAGAAGGAA

MLTHKNILLTIFGLFMIILSACGMSNKEMAGIDNWEHYQKEKKITIGFDNTFV
PMGFESRSGDYTGFDIDLNAVKEYGISVKWQPINWDMKETELNNGNIDLI
WNGYSKTAERAKVAFTPYPMNNHQVIVTKTSSHINSIKDMKGKQLGAQSG
SSGFDAFNAKPDILKKFVKKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANY
5 YLKQEG

Sequence description

10

A] Length: 649 bp - 216 aa (partial sequence)
B] TTG start codon is preceded by a possible
typical Shine-Dalgarno sequence. Has a
leader peptide

15

ID-154

20

Clone 2-c100

25

ATGAAAATTTGGAAAAAAATAACCTTAATGTTTCTGCAATTATTTAAC
ACAGTAATTGCATTGGGAGTCTATGTTGCCTCAGCTTATAATTTCGACTA
ATGAATTGTCTAAGACTTT

MKIWKKITLMFSAIILTVIALGVYVASAYNFSTNELSKTF

30

Sequence description

35

A] Length: 123 bp - 41 aa (partial sequence)
B] ATG start codon is preceded by a potential
typical Shine-Dalgarno sequence. Has a
typical leader peptide

40

ID-155

Clone 2-c1

5 ATGAAAAAACAAAGACTATTACTGCTTTGGAGGCTTATTAATAATGATA
 ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAA
 GGAATACCAAGGCAGAACAGAATTTAAGTCATACTTAAATATATATCAG
 ATAAAAAATAACTATTAGATAATATAAAAGTTATTACTTTCTATAAGTA
 TTTCTAAAGATGTACAAGATAAAGTCAGTGAAACAACAACCTGTTCATATA
 GACTAGAAAAGCAAAAGAATCAAGAGTTCATGGTAATTGAAACATGAA
 GTTAGTGAATCTAGTCATATTCAACCGAAGTTAAAAATCAAATACAGTAT
 CCAATCCAGTATAAAAGATAATTCAATTCTGTTACTGAAAAAACACCGTCA
 GAACGTTATGATGAGTTGTTAGTCATTGATTCTCATTATTAACAAA
 AATATAAAATATATGATTACTTACTAAAACATCCCGAAACTGAATTAAAA
 GGTGTTCTATAAGATTCTATAAAATTCTGAAATTGTAGCCCCTTTATAAA
 ATCAATTAAATATAAAACCTAAACATCATCTATTGGTTACAAAAAA
 CGGAAAGTAAAGAATATTATTATACAATCAGTATTGATACTGATTCTGAGA
 TATATTCTATATTCAAGGTATTCTAT

20 MKKQRLLLLFGGLLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYFKYISDKN
 NYLDNIKVYYFSISISKDVQDKVSETTCSYRLEKQKNQEFIGNFEHEVSESSQ
 YSTEVKNQIQYPIQYKDNSIRTEKTPSERYDEFVFSFDSSLLKKYKIYDYLK
 HPETELKGVSYKIPINSEIVAPPINQLNIKNPKKSSISVTKTESKEYYYTISIDTS
 EIYSIFEGIH

25 Sequence description

30 A] Length: 687 bp - 229 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 typical Shine-Dalgarno sequence. Has a
 typical leader peptide. C-terminus has yet to be
 verified

35 ID-156

Clone 2-c5

40 ATGACATTGACACCATTGATCAATTAGCGGTTAATACAGTCCGCACGCTT
 TCTATTGATGCTATCCAAGCAGCAAATTCTGGGCACCCAGGTCTCCTATG
 GGAGCTGCGCCTATGGCTTATGTGCTTGGAAATAAATTCTAAATGTAAAC
 CCAAAAACAAGTCGCAATTGGACAAACCGTGACCGTTGTACTTCAGCT

GGGCATGGTCAGCTCTTATAGCCTACTTCATTTAGCTGGCTATGATT
TATCAATTGATGATT

5 MTFDTIDQLAVNTVRTLSIDAIQAAANSGHPGLPMGAAPMAYVLWNKFLNVNP
KTSRNWTNRDRFVLSAGHGSALLYSLHLAGYDLSIDD

Sequence description

10

- A] Length: 272 bp - 90 aa (partial sequence)
- B] ATG start codon is preceded by a potential typical Shine-Dalgarno sequence. No obvious leader peptide

15

ID-157

20

Clone 2-c8

25

ATGAGAACACTATTTAGAATGATATTGCTATTCCAAAGTTATCTTTAGA
TTGATTGGAATATCATTGGGAATTCAAGACAGTTCTGTTATTGCG
ATTATTTATTGGCTTGTATTACTATGCGAATCACAGTCAATCAGAATTG
CTAATCAACTTAGTGACATTATCAGACAGGAAAAACATT

30

MRTLFRMIFAIPKFIFRLIWNIIWGIKTVLVIAILFGLYYYANHSQEFANQLS
DIIQTGKTF

Sequence description

35

- A] Length: 197 bp - 65 aa (partial sequence)
- B] ATG start codon is preceded by a potential typical Shine-Dalgarno sequence. Possesses a leader peptide

40

ID-158

Clone 2-c9

5

ATGTCAAAAAAAATAATATTAGGAATTTATCTCTTTATCTGTCGTTACTT
 TGGTGGCGTGTGGTTCATCAGACAAACAGCTACAAGATAAAGTTGAGAAA
 AAAGGGAAGTTAGTTAGCGGTGAGTCCAGATTATGCTCCCTTGAGTT

10

MSKKIILGILSLLSVVTLVACGSSDKQLQDKVEKKGKLVLAVSPDYAPFEF

Sequence description

15

A] Length: 153 bp - 51 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 typical Shine-Dalgarno sequence. Possesses a
 leader peptide (not in frame with nuc)

20

ID-159

25

Clone 2-c10

30

ATGAAAAATCAAAGACTATTACTGCTTTGGAGGCTTATTAATAATGATA
 ATGATGACAGCATGTAAGGATTCAAAAATCCCAGAAAACCGCACGAAAAAA
 GGAATACCAAGGCAGAACAGAAATTTAAGTCATACTTT

MKNQRLLLFGGLIMIMMTACKDSKIPENRTKKEYQAEQNFKSYF

35

Sequence description

40

A] Length: 139 bp - 46 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 typical Shine-Dalgarno sequence. Possesses a
 leader peptide

ID-160

Clone 2-c11

5

ATGATTGGAAAATTATATTATAGCTATAGAAAGTCACGCTTATTAAGAAGT
 ATTTTATGGCTTATTTAATTGTTGGTGTATATGTTAGGACAACGTGTT
 TATTATCCACTGTTCTTATCACATCAAGAGATAAAACTAGCAGTAGATC
 AACATTTACTCAATAACTTTCAGCAGTAAGTGGTGGGAGTTTAATAAAT
 TAAATGTTTCACACTGGGTTGAGTCCATGGATGTCAAGTATGATTATT
 GGAGATTGTTCTTATTCGTGGCAAAAAATGCAACGAAGCGAAAA
 GCAGAAGTAGCTCAATATACTTAATGCTTACTATCTCAGTTATACAAGCA
 TATGGTGTTCAGGAAATCAATTATAAAAGCTCTTATTAGGTTCTTATA
 15 GTGATATTGTTTT
 MIGKLYYSYRKSRLRSILWLILIVGVYMLGQRVLLSTVPLSHQEIKLAVDQHL
 LNNFSAVSGGSFNKLNVFTLGLSPWMSSMIIWRFVSLFSWAKNATKRKAEVA
 QYTLMLTISVIQAYGVSGNQFIKSSLGSYSIDIVF
 20

Sequence description

25

A] Length: 423 bp - 141 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 typical Shine-Dalgarno sequence. Possesses a
 leader peptide

30

ID-161

35

Clone 2-c13

ATGAAAGGTCTATTGGATTTAGTTAATATTGCCAGAACGCCAGCTATT
 40 TTAGTCGCCTTGATAGCCATTATCGGTTAGTACTGCAGAAAAAAGGTGTT
 CCTGATATTGAAAAGGTGGAATAAAAACATTGTTGGCTTCTAGTGGTT
 TCTGAAGGTGCAGGGATAGTCCAAAATTCTTGAATCCATTGGAAAAATG
 TTTGAACATGCTTTCATTGGTGGGGTAGTTCTAATAATGAAGCCATT
 GTAGCAGTAGCTCTTACGAAGTATGGCTCAGCAACTGCTTGATTATGTTA
 GCGGGAATGATTAAATATTTAATTGCTCGTTACAAAAA

MKGLLDFLVNIARTPAILVALIAIIGLVLQKKGVPDFVKGGIKTFVGFLVVSEG
 AGIVQNSLNPFGKMFEHAFHLVGVVPNEAIVAVALTKYGSATALIMLAGMI
 FNILIARFTK

5

Sequence description

10 A] Length: 348 bp - 116 aa (partial sequence)
 B] ATG start codon is preceded by a potential
 Shine-Dalgarno sequence. Possible leader
 peptide

15

ID-162

Clone 2-c21

20

TTGGTTGGTAAGCCCCAATTACTATTTTAGATGAACCTACTCCGGAATG
 GATACTTCCACACGTCAACGATTGGAAAGCTGGTTGCGACACTAAAAAA
 AGAAGGTGACACAATTGTCTATTCTAGTCATTATATCGAAGAGGTTAGAAC
 25 ATACAGCTGATAGGATTTAGTACTTCATAAAGGAAAGTTATTACGCGATA
 CAACCCCCTTGCCATGAAGCAAGAAAAACCGAAAAGTTATTACCGCGTT
 CCGCTTAGTTATCAAAAATTATTACCTACCTATTGATTACAGAGTGTGAA
 GCCAAGAGTGTAGTATAACGTTGTTACTGGGGAGGCTGAAACTGTATG
 30 GAAAATACTGGCAGATAATGGTTGTCTATTGAAGCTATTGAGATGACCA
 ATAGAACTTGTTAAATCGTATTTGAGACTACTAAGGAGGTAAAACATG
 AGAATCTTA

30

MVGKPQLLFLDEPTSGMDTSTRQRFWKLVATLKKEGDTIVYSSHYIEEVEHTA
 DRILVLHKGKLLRDTPFAMKQEKTKEKFTVPLSYQKLLPTYLITECEAKSDSI
 35 TFVTGEAETVWKILADNGCPIEAIEMTNRTLLNRFETTKEVKHENL

Sequence description

40

A] Length: 462 bp - 155 aa (partial sequence)
 B] Putative TTG start codon is not preceded by
 an obvious Shine-Dalgarno sequence. No obvious
 leader peptide. N- and C- termini require further

examination.

ID-163

5

Clone 2-c25

10 TTGAAAAAAATCCAAGAGAAGCCGTAAGGCAGTGACAACAAGTGGTGAGA
 AGACTTTACTTGAGGATTGGCAAAATGAATTCTCTAGACGAAGTCATTA
 ATGTTATGGTTTATATACCTTGAATAAGACAAAATCTGCTAACTTAAATA
 AGGCCTATATCATGAAAGTTGCTAATGATTTGCCTTCAGAATGTTATGA
 CGGCCGAAGATGCTGTGCTAAAATTCTGTGATTTTCAGATCAAAAAGTAA
 15 GGACTAAAACAGAAACGAAGAAGAAACAATCGAATGTTCTGAATGGAGT
 AATCCTGATTATAAGATGAGGTTAGCCCAGAAAAAGAAATTGAATTAGA
 ACAGTTT

20 MKKSKRSRKAVTTSGEKTLLEDLAKMNFLDEVINVMVLYTLNKTSA
 NLNKAYIMKVANDFAFQNVMTAEDAVLKIRDQKVRTKTETKKQSN
 PEWSNPDYKDEVSPEKEIELEQF

Sequence description

25

A] Length:360 bp - 120 aa (partial sequence)
 B] N- and C- termini require verification.

30

ID-164

35

Clone 2-c28

40

ATGACGAATCATATTACTAAACTGATAGAAAATAGCGGAAAAAAATTGAC
 AGAAATTAGCGAAGCTACAGATATAGCCTATCCTACACTTCTGGATACAA
 TCAAGGAATCCGCAAACCTAAAAAGATAATGCTGAAAATTGGCAAAAT
 ACTTTAATGTTCCGTCGCTTACATTATGGGACTTGATAGCAACCCACATG
 CTCCATCAAATCTT

MTNHITKLIENSGKKLTEISEATDIAYPTLSGYNQGIRKPKKDNAEKLAKYFNV
 SVAYIMGLDSNPHAPSNL

Sequence description

5

- A] Length:218 bp - 72 aa (partial sequence)
- B] ATG start codon is preceded by an obvious Shine Dalgarno sequence. No obvious leader peptide.

10

ID-165

15

Clone 2-c29

20

TTGATGAAAAGGAATAAACATTACCGTTAACAGAAACTACCTATTATATT
 TTATTAGCTTGTGAGGAAGCGCATGGCTATGCTATTATGAAAAAAAGTT
 GAAGAAATGAGTGGCGGTGATGTTAGAATAGCCGCAGGGACAATGTACGG
 TGCCATTGAAAATTACTTAAACAAAAATGGATAAAGTCTATCTCAAGTGA
 CGATAGAAGAAGAAAAGTTATATTACTGAGACAGGAAAAGAAATAG
 TAGAACTTGAAACGAATCGATTAAGAAAGTTACTTAATACTGCTAATCAGT
 25 TGGGTTTGGAGGAGATGGTTATGATAAAAGTT

25

MMKRNKHLPLTETTYYILLALFEEAHGYAIMKKVEEMSGGDVRIAAGTMYG
 AIENLLKQKWIKSISSSDRRKVYIITETGKEIVELETNRLRKLLNTANQLGFG
 GDGYDKV

30

Sequence description

35

- A] Length:337 bp - 112 aa (partial sequence)
- B] TTG start codon is preceded by an obvious Shine Dalgarno sequence. Actual start codon may ATG that comes immediately after the TTG. Potential leader peptide.

40

ID-166

Clone 2-c35

5 CCCATTACTGGTGAGTTAATAGCTGAGAAATTAGGAGTACCAAGAGCAGC
 ACTAAGGTCTGATTGCGGGTTTAAGTATGCTAGGTATCATAGATGCAAA
 ACCTAAGGTTGGTTATTTTATTAGGACAGTATCATGCTTCAATAGGGAC
 AAGTCATTTGAAAAGATGACAGTTAGAAATTATGGGGATCCTTCTGAC
 AGTTCATCAAAAAGATTCAAGTTATGATGTTATTGTACATATTTTATGGA
 10 AGATGCTGGTTGTGCTTTATCTTGGATGATGATGATGATTCTCTGTGGAGTC
 GTGTCACGTAAGATTACTAAAAACAGTATTGGCGGAGGAGATCTTCT
 AAAATGCCAATAGGAATGGTGATGACACGTATGCCACACGTGACAACGT
 TTTAGAAAATGAAAGTCTTTGCGGCAGCTGATAAAATTAGTGAGCAGAA
 AAGTGGATAGTCTCCCTGTCGTCATGATAAGCAATATCCGAAAAAT
 15 TTA
 PITGELIAEKLGVPRAALRSDLRVLSMLGIIDAKPKVGYFYLQYHASIGTSF
 EKMTVSEIMGILLTVHQKDSVYDVIVHIFMEDAGCAFILDDDFLCGVVSRKD
 20 LLKTSIGGGDLSKMPIGMVMTRMPHVTTVLENESLFAAADKLVSRKVDSLKV
 VRHDKQYPEKF

Sequence description

25 A] Length:511 bp - 170 aa (partial sequence)
 B] N- and C-termini to be determined

30 ID-167

Clone 2-44

35 TTGGAAGTCATCATGCAATTATTTATAGTATTATTGGTATTTATTGGTAT
 TAGGAATTGTGTATGCAATTCTTCAATCGTAAGAGTGTCTCTAAGTT
 AATTGGAAAAGCTCTTATCGTTCAATTCAATTGCGCTAATCTTAGTACGT
 40 ATCCCACTAGGCCAACAAAGTTGTTAGTGTGTTCAACTGGAGTTACTAAA
 GTAATCAACTGTGGTCAAGCTGGTT
 MEVIMQFIYSIIGILLVLGIVYAIISFNRKSVSLSLIGKALIVQFIIALILVRIPLGQQ
 VVSVVSTGVTKVINCQAG

Sequence description

5

A] Length:233 bp - 77 aa (partial sequence)
 B] TTG start codon is preceded by a possible Shine Dalgarno sequence. Actual start codon may occur further downstream. Potential leader peptide.

10

ID-168

10

Clone 2-46

15

CAACCTAATAAAAGCTTAGAAAGTGTGAGATTGATATTAAATGCTTCCAG
 CATTATAATTACTAACCAATTGGAATAAAGCAAATAAGACCAATCTTGTT
 TCCGTTGCTGAGACATACTTACTTCCTTAGATTATACTCTGGTACTAAGA
 20 ACGGTAAAGGTAAATACCAAAACAGTTCTGAAATTCCAATAAAGCAACT
 ATTACTATCCCAAACGATGCAGTTAACGAAAGTCGCTCTACTTGTAA
 CAATCAGCAGGCTTGCTAAAATTGAAAGTATCAGGTGATACATTAGCAAC
 AATGTCAGATGTTGTTCCAATCCTAAATCTTAGATT

25

QPNKALESDEIDINAFQHYNLTNWNKANKTNLVSAETYFTSFRLYSGTKN
 GKKGKYQTVSEIPNKATITIPNDAVNESRSLYLLQSAGLLKLKVSGDTLATMSD
 VVSNPKSLD

30

Sequence description

35

A] Length:344 bp - 114 aa (partial sequence)
 B] N- and C- termini require verification

ID-169

40

Clone 2-47

ATGAAATGTATAATAATAATATAAATAAAATAAAATGATAATTGAGAT
 TTATCATAGAAGGAAAATCTTTGAAATTAAATAATCATATTATCTAC

TGCAGCTCTTACTGCTCTTTAGGATATAATAGCGTTACTGCGGATACA
 TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAACTGAGGA
 ATATAACTATAATAACCAGATAGAACCTCAGGAGCGTATAAAAAACCTAA
 ATATACCTTT

5

MKCIINNINKIKMIIIEIYHRRKTILKLNKILSTAALTALFLGYNSVTADYN
 QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

10 Sequence description

A] Length:264 bp - 88 aa (partial sequence)

15

B] There is a Shine-Dalgarno sequence upstream
 of this sequence. Potential leader peptide
 sequence

20 ID-169

Clone 2-47

25

ATGAAATGTATAATAATAATATAAATAAATGATAATTGAGAT
 TTATCATAGAAGGAAAATCTTGAATTAATAAATCATATTATCTAC
 TGCAGCTCTTACTGCTCTTTAGGATATAATAGCGTTACTGCGGATACA
 TATAATAACTATCAGCCACATAGATCAAATAATATGGATTTAACTGAGGA
 ATATAACTATAATAACCAGATAGAACCTCAGGAGCGTATAAAAAACCTAA
 ATATACCTTT

30

MKCIINNINKIKMIIIEIYHRRKTILKLNKILSTAALTALFLGYNSVTADYN
 QPHRSNNMDLTEEYNYNQIELQERIKNLNIPF

35

Sequence description

40

A] Length:264 bp - 88 aa (partial sequence)

B] There is a Shine-Dalgarno sequence upstream
 of this sequence. Potential leader peptide
 sequence

ID-170

5 Clone RS-58b

TTGGGTGATTATTATGGTAAGAAATTTGGTGANAGCAGCTAAAAAGA
 CGTCGAACATATGGCTAAGAAAATCATTAATGTCTATAAACACGGTTAA
 10 AAAACAAACACTTGGTTATC
 AGAAAATACAAAAGCAATGCCATTAGAAACTTGATAACATGAGATTAA
 TGATTGGCTATCCAGAAGATTATCCTGATCTTATCGTCAGTACCAATTG
 ATAGTAAAGCAAGCTTCTTGAAAACAATGATAACTACAGAAAATTATCG
 15 ACAAGAAAACATTGAAGAATTAAACCAAGTCTAACACGTGAACATTG
 GCAAATGAGTGCCAATGCTGTAATGCTTATAATGATCCTAACACCAATTG
 CATACTCTTCCAGCAGCGATTTCATCACCACTGTACGATAAAACTAA
 AACAGTTAGTCAAAATTATGGAGCTATGGAGCAATTATGGTCATGAAAT
 TTCACACTCATTGATATTAAATGGTATGAAATATGACGAGAAAGGGAAATCT
 20 TCACGATTGGTGGACTAAAGAAGATTAAATCATTATAAGAAATCAACAC
 AAGCTATGATTGACCAATGGGATGGCCTAAAGCAGATGGCGGTAAAGTT
 GATGGTAAATTAACTTAGCAGAAAATATTGAGATAATGGGGTTATG
 GCATCTCTAGAAGCTCTAACAGACTGAAAAAAATCCAAACTATAAGAATT
 TTGAATCATGGCAAGTATTGGCGTCAAAAGCAACCAAGAACAAAGT
 25 AAGTCCTCAATTCACTGAGATGTTCATGCACCATATGAATTGA >
 GAGCTAACATCCCAGTACGTAATTCCAAGAATTATGATGCCTTGGTG
 TTAAAAAAGGCATTCAATGTATCTAAAACCAGAAAAACGTTGACACTT
 GGTAA

30 MGDYYGKKYFGEAKKDVEHMAKKIINVYKTRLKNNTWLSENTKAMAIKK
 LDNMRLMIGYPDYPDLRQYQFDKSASFFENNDNYRKLSNKKTFEFNQSNQ
 REHWQMSANAVNAYNDPNTNSIVFPAAIFQSPLYDKTKTVSQNYGAIGAIIGH
 EISHSFADINGKYDEKGNLHDWWTKEQLNHYKKSTQAMIDQWDGLKADGG
 KVDGKLTLAENIADNGGVMASLEALKTEKIQTICKNFLNHGQVFGVKKQPKNK
 35 VSPQFSQMFMHMN*

Sequence description:

40 A] Length: 819 bp - 272 aa (full length gene)
 (107 bp of additional DNA sequence (> onwards) is
 also included. While not in-frame with the
 described orf, it also shares strong homology
 with the neutral peptidases.

5 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-89 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-89 gene sequence. ID-89 and ID-170 together show homology over their combined entire length with the neutral endopeptidases from *Lactococcus* and *Lactobacillus*. Possesses TTG (possible ATG start codon located 13 bp further downstream) start codon with no obvious signal peptide. Shine Dalgarno sequence not immediately obvious. Possibly located further downstream

10 ID-171

Clone 2-18/22b (Mod2)

15 ATGACCATGATTACGCCAAGCTTCATTAAGGTATCTCTAGATGAAACAAAT
 CGTATGATGCGTATGATATCAGATTATTAAGTTATCGCGCATTGATAAT
 GAAGTAACGCATTTAGATGTTGAAATGACGAATTTCACAGCTTCATGACC
 TCAATTGAAATCGATTGATCAGATTAGAAATCAAAAAACAGTCACAGG
 20 AAAAGTTTATGAAATTGTCAGAGATTATCCTCTTAAGTCAATTGGGTGGA
 AATTGATACAGATAAGATGACTCAAGTGATTGATAACATTAAATAATGC
 AGTCAAGTATTCAACCAGATGGTGGTAAGATTACAGTTAATCTACGCACAAC
 TAAAACGCAGATGATTATCAATATCAGACCAAGGCTAGGTATTCCCAA
 25 AAAAGATTACCTCTCATTTTGATCGTTTATCGTGTGATAAGGGCGAGA
 AGTCGTCAACAGGGTGGGACTGGACTTGGTTGTCAATTGCAAAAGAAAT
 TGTAAAGCAGCATAAGGGATTATTGGGCTAAGAGTGAGTATGGTAAAG
 GGTCTACTTTACAATCGCTTGCCTATGATAAAAGATGCTGTAACATTATGA
 AGAATGGGAGGACGTTGAAGATTAA

30 MTMITPSFIKVSLDETNRMMRMISDLLSLSRIDNEVTHLDVEMTNFTAFMTSIL
 NRFDQIRNQKTVTGKVYEIVRDYPLKSIWVEIDTDKMTQVIDNILNNAVKYSP
 DGGKITVNLRTTKTQMILSISDQGLGIPKKDLPLIFDRFYRVDKARSRQQGGTG
 35 LGLSIAKEIVKQHKGFIWAKSEYKGSTFTIVLPYDKDAVTYEEWEDVED*

Sequence description:

40 A] Length: 613 bp - 212 aa (full-length gene possibly)
 B] Possible Shine Dalgarno sequence present
 upstream of a ATG start codon. May not have yet
 determined the N- portion of this gene. No
 obvious signal peptide.

ID-172

5

Clone 2-54balternate (107b)

10 TTGAAAAAAATTATTACTTCTATTCTATTACTTAGTGCATTTTTATGC
 CAACCATCTCTGCTGAATCTTTAATGCTTCCGCTAAACATGCCTAGCAGT
 TGATTAGATTCAAGGAAAAACTTGTATGAAAAAGATGCTAACAAACCG
 CTGCTATTGCTCCTTACTAAAATAATGACCGTTATATGGTCTATAAAG
 AAATTGATAACGGTAACCTCAAGTGGAATACCAAAGTAAATATCTGAC
 TACCCTTATCAACTAACACCGAATCTGATGCTAGTAATGTTCTTAGAA
 15 AAAAGGCCTATACTGTTAAACAACTCGTGGACGCTGCCATGATTCTAGT
 GCTAACAGTGCAGCCATTGCTTAGCTGAACATATTCAGGAACGTGAAAGT
 AAATTGTTGATAAAATGACTGCTCAATTGAAAAGTGGGGATTATGAT
 AGCCACCTAGTCAATGCTCTGGCTAAATAATAGTATGTTAGGCAATCAC
 20 ATTTATCCAAAATCGTCACAAAACGACGAAAATAAAATGAGTGCACGTGA
 TATTGCTATTGCTGCCTACCATTGGTCAACGAATATCCTTCAATTCTAAG
 ATTACTAGTAAGTCCGTTGCTAAATTGATAAAAGATATTATGCATTCTTAT
 AACTACATGCTACCAGATATGCCTGTCTTAGCAGGTTACAGGTTG
 25 AAAACTGGGACAACGGAATTAGCTGGCCAATCTTTATTGCTACATCTACT
 GAAAGTGGATGAGACTACTCACTGTTATTATGCATGCTGATAAGGCCGAT
 AAAGACAAATATGCTCGCTTACAGCAACTAACTCTCTTGAACATATAC
 ACAAACACCTACGAACCTAACCTGTATTAGCTAAAGGAGCTGCATATAA
 AGGTAAAGAAGCAAGTGTGAGAGACGGAAAAGAACAAATCGGTATCGCT
 GTTGCTAAAACGATTGAAAGTAGTACAGAAGAAAAATATCACTAAACA
 30 AAATCAGTTAAAATTAACTTAAAAAGAGCTTACTGCTCTTATTACAAA
 AAAAGAGAACCTAGGGAAAGCTTATTACGTTGACCTTAATAAGGTTGGAA
 AAGGCTATCTCATAAAGGAACCTAGCGTTCAATTAGTGGCAAAAGATAGT
 ATTGAGCGCAGTTCTCCTCAAAGTGTGGTGAATCATTGTGCGCTAC
 GTTAACGAAAAACTTAA

35 MKKIITSILLSCIFFMPTISAESFNASAKHALAVDLDSGKILYEKDANKPAAIA
 SLTKIMTVYMVYKEIDNGNLKWNTKVNISDYPYQLTRESDASNVPLEKRRYT
 VKQLVDAAMISSANSAAIALEHISGETSKFVDKMTAQLEKWIHDSHLVNA
 SGLNNMSLGNHIYPKSSQNDENKMSARDIAIAAYHLVNEYPSILKITSKSVAKF
 40 DKDIMHSYNYMLPDMPVFRPGITGLKTGTTELAGQSFIASTESGMRLTVIM
 HADKADKDKYARFTATNSLLNYITNTYEPNLVLAKGAAYKGKEASVRDGKE
 QSVIAVAKNDLKVVQKKNITKQNQLKINFKELTAPITKKENLGKAYVVDLN
 KVGKGYLIKEPSVHLVAKDSIERSFFLKWWWNHFVRYVNEKL*

Sequence description:

5 A] Length: 1236 bp - 412 aa (full-length gene sequence possibly)
 B] A possible Shine-Dalgarno sequence precedes the putative 'TTG' start codon. (needs further cloning and sequencing to verify N-terminus)

ID-173

10

Clone 3-60b

15 ATGACGCTTCGAGAATTAACAATAGAAGAACATTAAAGAACATTAGGAAA
 TTATGATTACAATCATTTCACAAACACCTGAGATGGCTAAACTTTAGA
 AAAACGCGGCTATGATGTTAGGTATTGGGATATCAAGTAGAAAATAAAC
 TAGAGATAATCAGTTATCTTATATTATGCCAGTCACTGGTGGTTCAAAT
 GAAAATTGATTCAAGGACCAAGTTCATTCAAATTCTAAGTATCTAAAACAATT
 20 TTATAAAGCATTGCAAGGCTATGCCAAATCCAACGGTGGTTCTAGAATTAAAT
 AGTTGAGCCTTTGATGATTACCAATTATTCACTAGTTGGGAGTTCTAGT
 AATCAGGGAAATGATAATCTGATTGAAGATTTCACAGTTCAAGGTATCAC
 CATGATGGTTAACAACTGGTTACTGGTAAATATTATCTGGCACTATG
 TTAAAAATTAGAAGGTGTCACCTCTGAAACGTTACTATCTTCATTCTCTAA
 25 GACAGGACGAGCTTGGTTAAGAAAGCAATGTCTTTGGAATCAAGGTT
 GCGTTCTAACGTGATGAGCTACATTATTAAAGAGATAACAACTTCTA
 CGTCAAATAGACGTGATTATATGGATAAGTCCTAGATTATTATCAAGATT
 TTTACGATAGCTTGAAGGCAAGGCTGAATTGTGATTGCCACTTAAATT
 TTAGAGAATACGACCATAACTGCAAATAAAAGCTGAAGCATTGGAAAAT
 AAGCTT
 30

MTLRELTIIEFKEHSGNYDSQSFLQTPEMAKLLEKRGYDVRYLGYQVENKLEI
 ISLSYIMPVTGGFQMKIDSGPVHSNSKYLQFYKALQGYAKSNGVLELIVEPF
 35 DDYQLFTSSGVPSNQGNDNLIEDFTSSGYHHDGLTTGFTGKYLSWHYVKNLE
 GVTSETLLSSFSKTGRALVKKAMSGFIKVRLKRDELHLFKEITTSTSNNRDY
 MDKSLDYYQDFYDSFEGKAEFVIATLNFRDYHNLQIKAEEALENKL

40

Sequence description

A) Length: 771 bp - 257 aa (partial gene sequence)
 B) This gene sequence was not identified using the LEEP system. It was identified immediately downstream of the ID-65 gene which was identified by

5 LEEP, during cloning and sequence analysis of the full-length ID-65 gene sequence. Sequence Characteristics:
 No obvious leader peptide sequence
 Orf is preceded by a potential Shine-Dalgarno sequence.

10 ID-174
 Clone 2-17b (ID-80b)

15 TTGTCAATTAGTTGGTTGCAGTGTAAATCTTATCCCTCTAAAATCATGG
 GATCAGTTATTGATGCTATTACAACCTGGAAAATTAAACAAGACCACAATTAC
 TATGGAATTATTAGGTTGGTTGTCAAGCTTAGCTATGTATGGGCTGCG
 TTATATTGGCGTATGTATATTAGGGACTCTTACAAATTAGGCCAAGTT
 GTCAGATACCGTTATTGAACATTACAAAAATGTCTCCTCTTTATC
 AGAAATATCGTACAGGTGATTAAATGGCGCACGCACCAACGACATCAAT
 20 TCTCTAACACGTCTTGCAGGAGGGAGTTATGTCAGCAGTGGATGCCTCT
 ATCACAGCATTAGTAACGCTTATCACCATGTTCTTACTATTCGTGGCAA
 ATGACATTAATTGCGTTATCCCTTGCCTTAATGGCCTAGCACTAGTA
 AATTGGGGCGAAAAACCCATGAAACCTCAAAGAATCTCAGGCAGCCCTT
 25 TTCAGAATTAAATAATAAGTG
 30 MSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYI
 WRMYILGTSYKLGQVVRYRLFEHFTKMSPSFYQKYRTGDLMAHATNDINSLT
 RLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALALVNWGEK
 PMKPSKNLRQPFSELNNKV

35 Sequence description
 A) Length: 534 bp - 178 aa (partial gene sequence)
 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-80 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-80 gene sequence.
 Sequence Characteristics:
 40 No obvious leader peptide sequence
 Orf is preceded by a potential Shine-Dalgarno sequence.

ID-175

5 Clone 2-11Ab (ID-103b)

ATGCATATTGAGACTTTATTGATTCAAAGAATTAGGAAAAAGATATCGT
 10 TTTAAAAATCCTACAAAAGAATTAATAGCTGATACTTAGAACAAAGCTTA
 GAAGTGATAAAAGAAGTTGATTATTATCAATCTCAAAATTATTATGTTGTT
 GTTATTATCTTATGAAGCATCTGCTGCTTGTGATTACATTAAAGTT
 15 CTCAACAGAAGTTGGCTGGAGAACATCTAGCTTATTTACAGTACATAAAG
 ATTGTGAGAACGAAGCTTCCTTAAGTTATGAAAATGTTAGATTAGCAG
 ATAATTGGACTGCTAATGTTCTGAGCAAGAACATCAAGAGGCAATTGCTA
 ATATTAAAGGACAAATTAGACAAGGAAACTTATCAAGTAAATTATACA
 CTAGAGCTTAGCCAACAATTATGCTCGGATCC

20 MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYVVGY
 LSYEASAAFDSHFKVSQQKLAGEHLAYFTVHKDCENEAFPLSYENVRLADNW
 TANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSD

25 Sequence description:

A] Length: 440 bp - 146 aa (partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-103 gene which was identified by LEEP,
 during cloning and sequence analysis of the full-length ID-103 gene sequence.
 30 Shine Dalgarno sequence present upstream of
 ATG start codon, No apparent leader peptide sequence

ID-176

35

Clone 2-18/22b(b) (ID-104b)

40 GTGAATAATATGTTTATCTAAAATAGCCTGGCATAATTAAAACATTCT
 ATAGACCAGTACATACCATTCTCTTAGCCAGTTATTACTTATTCAATTGA
 CTTGTTCTACGCTACTAATCTTAAATGAGTGCTGTTGGAAAGAGATATGGGA
 CAGCGGCAACGGTCTTTCTTGGAGTGATTGTTGTCAATCTTGCCTG
 AGTCATGGAACATTATAGCTACAATATCTTGTGAAACAGCGTAGTAGTG

AATTGGACTGTATAACATTTGGGATGAATAAACGTCAAGTGCACGTG
 TAGCTAGTCTAGAGCTGTTATTATTTATTTCTTATTCATAAGGAAG
 TCTGTTAGTGCCTTTGCTAAATTATTAATTGTCAACATTA
 5 TTAACATATCATGCACTAAATCTTAGTTAAGTTATGGCCATTATTATTG
 TATCGTTATATTACAGGTATTCTGACTTAAAGTCCAGTTATCGA
 CATGTTCATTTATCATCCCCATTAAGTCTTTAGAAAGAAACAACAGGGA
 GAAAAAGAACCAAAAGGTAACTTATACCGCTTACTTCAGGTAAAGCACCTGCATTA
 ATCGCCATCGCTTATACAATGGCTTACTTCAGGTAAAGCACCTGCATTA
 GCTGTTATCTATCGTTCTTGCAGTACTTTAGTAATTGCTGGTACTT
 10 ATCTTTTATATTAGTTATGACATGGTACTAAAAAGGTGCGTCAAAA
 CAAGCATTATTATTATAAAATCTGAGCATTTGTATCAACTCGCAAATGAT
 TTTTCAATGAAGCAAAATGCAGTAGGGTTAGCAAGTATCACTTATTAGC
 TGTTATGGCTCTAGTTACTATTGCTACAAACAGTCTCACTCTATTCAAATACA
 15 CAAAATGTTGTTACCGGACTATTCCAAAATCAGTAAGTTATCAATAGAT
 AATTCAAAAGGTGACGCGAAAAATATATTGAAGAAAAGATTGAAAGAA
 ACTAGGTAAGTCATCTAAGGAAGCTACTTATAATCAGACAATGATTTC
 GATGCCAGTTAGTCAATCAAGTGAECTTAATATCACATCTA

20 MNNMFYLKIAWHNLKHSIDQYIPFLLASLLYSLTCSTLLILMSAVGRDMGTA
 ATVLFLGVIVLSIFAVVMEHYSYNILMKQRSSEFGLYNILGMNKRQVARVASL
 ELFIIYIFLISIGSLFSAFFAKFIYLIFVNIINYHALNLSLWPFIICIVFTGIFLTLE
 VPVIRHVHLSSPLSLFRKKQQGEKEPKGNLILAILALVIAIAYTMALTSKAP
 25 ALAVIYRFFFAVLLVIAGTYLFYISFMTWYLKRLRQNKHYYKSEHFVSTSQM
 IFRMKQNAVGLASITLLAVMALVTIATTVSLYSNTQNVVTGLFPKSVSLSIDNS
 KGDAKNIFEKILKKLGSSKEITYNQTMISMPVSQSSDLISHL

30

Sequence description:

35 A] Length: 1119 bp - 373 aa (partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified upstream of the ID-104 gene which was identified by LEEP, during
 cloning and sequence analysis of the full-length ID-104 gene sequence.
 Possible Shine Dalgarno sequence present
 upstream of a GTG start codon. Possesses a potential
 40 leader peptide sequence

ID-177

Clone 2-5b (ID-112b)

5 ATGGTTGAGCCAATTATTCATAACAAGGACTTCATAAAAGTTTGGGAAA
 AATGAGGTTTAAAAGGCATTGACTGGATATTCAAGGAGAAGTGGT
 GGTTATTATTGCCCTCTGGCTCTGGTAAGTCACACATTAAAGAACAT
 GAATCTCTGGAAAGTACCAACAAAGGGAACAGTGACTTTGAAGGGATTG
 ATATAACAGACAAAAAGAATGATATTAAATGCGCGAAAAAATGGC
 10 ATGGTTTTCAACAGTCAATCTATTCCCAATATGACTGTACTAGAAAAT
 ATTACTTATCACCTATTAAGACAAAGGGACTTCTAAGCTTGATGCTCAG
 ACAAAAGCATACGAGCTATTGAAAAAGTTGGACTCAAAGAGAAGGCTAA
 TGCTTATCCAGCAAGCTTATCTGGAGGACAACAACACGGATTGCTATTGC
 AAGAGGTCTTGCATGAATCCTGATGTCCTTGTGAACTGCAAGATTAA
 15 GCTCTTGATCCTGAAATGGTAGGTGAAGTCTGACTGTTATGCAAGATTAA
 GCTAAATCTGGTATGACGATGGTATTGTCACTCATGAAATGGGTTTGCA
 CGTGAAGTAGCGGATCGTGTCAATTATGGATGCGAGGGATTATTGAG
 CAAGGGACCCCTAAGAAAGTATTGAGCAGACAAAAGAAATCCGCACAAG
 AGACTTCTTAAGTAAAGTATTATAA
 20
 MVEPIISIQGLHKSFGKNEVLKGIDLDIHQGEVVVIIGPSGSGKSTFLRTMNLL
 VPTKGTVTFEGIDITDKNDIFKMREKMGMVQQFNLFPNMTVLENITLSPIKT
 KGLSKLDAQTKAYELLEKVLKEKANAYPASLSGGQQQRIAIARGLAMNPDV
 25 LLFDEPTSALDPEMVGEVLTVMQDLAKSGMTMVIVTHEMGFAREVADRVIF
 MDAGIIVEQGTPKKVFEQTKEIRTRDFLSKVL*

30 Sequence description:

A] Length: 735 bp - 244 aa (full length gene)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-112 gene which was identified by LEEP,
 35 during cloning and sequence analysis of the full-length ID-112 gene sequence.
 Shine-Dalgarno sequence precedes the 'ATG'
 start codon. No obvious leader peptide

40 ID-178

Clone 2-5c (ID-112c)

5 ATGTCTCAsTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATT
 AAGTCAGATTAGAAGCTATTAAAGGAGATGAATCTGAAATTCAGGATCG
 TTTTACAAAACATTAGAATTGGAACGGCGGGATTGAGAGGTAAACTTG
 GAGCAGGAACCAATCGTATGAATACTTATATGGTGGGGAAAGCAGCACAA
 GCATTAGCTAATCGATTATTGATCATGCCCTGAAGCTATTGCACGTGGAA
 TTGCAGTTAGTTATGATGTCCCCTATCAATCTAAGGAATTGCAGAATTA
 ACTTGGTCCATTATGGCAGCAAATGGTATTAAAGCCTATATTAA

 10 MSHMNYKEIYQEWLENDSLGKDIKSDLEAIKGDESEIQDRFYKTLEFGTAGLR
 GKLGAGTNRMNTYMGKAAQALANRLLIMALKLLHVELQLVMMMSRYQSKE
 FAELTWSIMAANGIKALYL

15 Sequence description:
 15 A] Length: 366 bp - 122 aa (partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-112 gene which was identified by LEEP,
 20 during cloning and sequence analysis of the full-length ID-112 gene sequence.
 Shine-Dalgarno sequence preceded the 'ATG'
 start codon. No obvious potential leader peptide sequence.

25 ID-179
 25 Clone 2-5d (ID-112d)

30 ATGCAACCTGTAAAAGTCGATGAACCTCTGTTGAAGAAACCATTACTATT
 TTGAAAGGTATCCAAAAAAATACGAAGATTATCATCACGTAAAATATAA
 TAATGATGCCATAGAACGAGCTGCAGTACTATCTAACCGTTATATCCAAGA
 CCGCTTTTACCTGATAAGCAATAGACTTATTAGATGAAGCTGGTTCTAA
 AATGAACCTAACACTAAATTGTTGATCCAAAAGAAATTGATCAACGTCT
 35 CATTGAAGCAGAAAATTAAAAGCGCAAGCGACTCGTGAAGAAGATTACG
 AACGTGCAGCTACTCCGTGACCAGATTGCAAAATATAAGAAATGCAG
 CAACAAAAGGTCGACGATCAAGATAACACCTATTATTACGAAAAAACAAAT
 TGAGCACATCATTGAAGAAAAAACGAATATCCCTGTTGGTATTAAAAG
 AAAAGAACAACTCAATTAAATTCTCGCAGATGACTGAAACAGCAT
 GTGATCGGCCAGGATGACGCTGTCAATTAGATTGCAAAAGCTATTCGTCGT
 40 AATCGAGTTGGTCTTGGTAGCCAAACCGCTCTATTGGTTCCCTTTATTG
 TAGGACCAACCGGTGTGGTAAACTGAACCTCTAAACAAACTAGCAATTG
 AGCTCTTGGTTCAGCTGATAGTATGATTGCTTGTATGTCAGAGTACAT
 GGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGG
 GATACGAGGAAGCTGGACAAACTAACTGAAAAGGTTCGTCGAAATCCTTAC
 TCGCTCATCCTCTAGATGAAATTGAAAAAGCTCATCCGATGTCATGCAT

ATGTTCTTGCAGGTCTTGATGACGGTCATTAACAGATGGACAAGGAAG
 AACTGTTAGTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTC
 TGGTAAAACGTGAAGCAAGTGGCTTGCTCACGAGAAGGTAGGA
 CGAATTGAGCTCGGTACCCGGGATCCTAGAGTCGACCTGCAGGCAT
 GCAAGC

5

MQPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDIAIEAAAVLSNRYIQDRF
 LPDKAIDLLEAGSKMNLNTNFVDPKEIDQRLIEAENLKAQATREEDYERAAY
 FRDQIAKYKEMQQQKVDDQDTPPIITEKIEHIIIEKTNIPVGDLKEKEQLSQLINL
 10 ADDLKQHVIGQDDAVIKIAKAIRRNVRGLSPNRPISFLFVGPTVGKTELSK
 QLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRR
 NPYSLILLDEIEKAHPDVMHMFLQVLDDGRLTDGQGRTVSFKDIIIMTSNAGS
 GKTEASVFGASREGRTNSSVPGDPLESTCRHAS

15

Sequence description:

20 A] Length: 1070 bp ÿ 356 aa (Partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified upstream of the ID-112 gene which was identified by LEEP, during
 25 cloning and sequence analysis of the full-length ID-112 gene sequence. Shine-
 Dalgarno sequence preceded the 'ATG'
 start codon. No obvious potential leader peptide
 sequence.

ID-180

30 Clone 2-7b (ID-113b)

ATGAGAGGGAAGGTTATTAACGGCACAAACCTTATAGGTCTTTCTATT
 35 TTATTTCTATTTGGATTCTAACGATCACATCGAGAGAACATCATC
 ATCGTATAAACGAGGTAGATGCGAAGAGTGATTAAACAGGATTAAAACC
 CATTGCCATTATCAGCATTGATAACAAAGCAACAAGTTATTCTCTTGT
 ACAAAAGAAGGCGGAAATATGTCAAAGCTAGGGATAATATTAATGTTGA
 TATCGAATTACGGGATTCTCCAAGTAGATCACATCATTATCAGAAAAGCC
 40 GAGAATTAGGACAAAAGGGTTAATATCATATAGAGGAAATTCTCTCGTT
 ACTTGATAAGAAGTCATTGAAAGTTAAGTTGTTACTAATAAGTTAAAGG
 AAAAGAAGCATCGATTAGCAGGAATGCCTAAAGAACATCGGAGTGGGTATTG
 CATGGTCCCTTCTAGACAGAACATTATTAAGAAATTATCTGAGTTATAAT

ATTGCTGGT GAGATTATGCCTATGCCCAAACGTTCGCTACTGTGAGTTAT
TTGTCAATGGT GAGTATCAGGGAG

5 MRGKVIYGTTLIGLFLFFYFWIPKHHIERIHHRIKQVDAKSDLTGFKTHLPPI
SIDTKQQVIVPLVTKEGGKYVKARDNINV DIELRDSRSRSHLSEKPRIRT KGLIS
YRGNSRYFDKKS LKVFKVTNKLKEKKHRLAGMPKESEWVLHGPFLDRTLLR
NYLSYNIAGEIMPMPQTATVSYLSMVSIRE

10

Sequence description:

15

A] Length: 582 bp - 194 aa (Partial gene sequence)
B] This gene sequence was not identified using the LEEP system. It was
identified downstream of the ID-113 gene which was identified by LEEP,
during cloning and sequence analysis of the full-length ID-113 gene sequence.
ATG start codon is preceded by a Shine-Dalgarno sequence-Possesses a potential leader peptide
sequence. C-terminus to be determined.

20

ID-181

25

Clone 2-17b (ID-117b)

30

CTTCACATTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCT
TATTAGTGGATATTATTCAATGTATGTCTGCAGACCTTAATTCAATAT
TTTGGGAATCTCTTTGCGCGTGTCTTATAGTATTGTTAGAGATATT
GTAGAGATGCTTGCTAATATGAAAGGCTAGGCATGTCTTATTTGATA
GGACACCGGCAGGATCTATTGTGTACGTATTACTAATGATACTGAAGCAA
TATCTGATATGTTTCCGGTATTTATCAAGTTATCTCGGGATATT
35 TTTACAGTTACTCTGTACACTATGTTGATGCTAGACATTAACACTAACAGG
ACTCGTCGCTCTTGTACCTGTTATCTTATATTAGTGAATGTCTATCGG
AAAAAAATCAGTCAGTCACTGCTAAACGAGAAGTTACTTAGTGTATATC
AACAGTAAATTATCAGAAAGTATTGAAGGAATTC

40

SHFIDHYLTNVNQTAVLILVGYYSMYVLQTLIQYFGNLFFARVSY SIVRDIRD
AFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYT
MLMLDIKLTGLVALLPVIFILVN VYRKKS VTVIAKTRSLSDINSKLSE SIEGI

Sequence description:

5 A] Length: 498 bp - 165 aa (Partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-117 gene which was identified by LEEP,
 during cloning and sequence analysis of the full-length ID-117 gene sequence.
 N- and C-termini have yet to be determined

10

15 ID-182
 Clone 3-8b (ID-120b)

20 ATGTACCATATTGAATTAAAAAGGAAGCTTACTACCAAGAGAACGCCT
 AGTTGATTAGCGCAGATAGATTGAGTAATCAGGAGTTATTAGCCATTCT
 CTTACGTACAGGTATTAAAGAAAAACCTGTTCTGAAATTCAACGCAAAT
 TTTAGAAAACATAAGCAGTTAGCAGATTGGTCAATTATCCTTACAGGA
 GTTGCAATCCATTAAAGGAATCGGTCAAGGTTAAATCCGTCGAAATAAAAG
 CTATGCTAGAACTAGCAAAACGGATTACAAAGCTGAATATGATCGTAAA
 GAGCAAATTAAAGTAGTGAACAATTAGCGAGGAAAATGATGCTCGAATT
 AGGGGATAAAAAACAAGAACATTAGCTATTATGGATACACAAA
 ATCGTATTATCGAACAGAGAACTATTATTGGTACTGTACGTCGTCAG
 TAGCAGAGCCAAGAGAAAATTCTACATTATGCTTGTAAAAACATGGCAACT
 TCTTGATTATTATACATAATCATCCCTCAGGTTCTCCAATCCAGTGAAA
 GTGATTAAAGTTCACTAAAAAAATAAAACGATCATGTGATCATCTGGAA
 TTGTCTGCCTAGATCACATCATCGTTGGAAAAATAAATATTATAGTTTC
 GAGAAGAACAGATATTATAA

25

30

35 MYHIELKKEALLPRERLVDLGADRLSNQELLAILLRTGIKEKPVLEISTQILENI
 SSLADFGQLSLQELQSIKGIGQVKSVEIKAMLELAKRIHKAEYDRKEQILSSEQ
 LARKMMLELGDKKQEHLVAIYMDTQNRIIEQRTIFIGTVRRSVAEPREILHYAC
 KNMATSIIHNHPSGSPNPSESDLSFTKKIKRSCDHLGIVCLDHIIVGKNKYYSF
 REEADIL*

40 Sequence description:

 A] Length: 681 bp - 227 aa (full-length gene)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-120 gene which was identified by LEEP,

5 during cloning and sequence analysis of the full-length ID-120 gene sequence. ATG start codon is preceded by an typical Shine-Dalgarno sequence. No obvious leader peptide sequence

5

ID-183

10

Clone 3-11b (ID-121b)

15

TGGTTAAAAGTAGTGATAGCTTGTATTCCATCTATTTAATTGCTTACCAT
 TTGATAATTGGTTGAAGCTCATTAAATTGATTCGATTGCAATAGC
 CCTAATCTTTATGGTTTGTCTCATATGGGTTGAAAAACGTAATGCACAC
 CTCAAACACAGGTAAACGAATTGGCAAGTATGTCTTACAAGACAGCTTTC
 TTGATTGGATGTTCCAGGTTCTCAGTATTGTTCCGGGAACCAGTCGTTCTG
 GAGCTACTATTTAGGAGCAATTATTATTGGAACACTAGTCGTCGGTCGCTG
 20 CTGACTTTACTTCTTCTTGCCATCCCAACTATGTTGGTTATAGTGGACT
 TAAGGCAGTTAAATATTTTAGATGGTAACGCTTGAGTTAGACCAATC
 TTTAATACTTTAGTAGCAAGTCTGACAGCTTCGTAGTTAGTTATATGTT
 ATTCGTTCTTGACAGACTATGTCAAACGACACGATTCACCATTTGGT
 25 AAGTATCGTATAGTCTTAGGAAGTTACTCATCCTCTACTGGTTAGTTGTC
 ATTATTCTAA

25

WLKVVIACIPSILIALPFDNWFEAHNFMIPIAIALIFYGFVFIWVEKRNAHLKP
 QVTELASMSYKTAFLIGCFQVLSIVPGTSRSGATILGAIIGTSRSVAADFTFFLA
 30 IPTMFGYSGLKAVKYFLDGNVLSLDQSLILLVASLTAFFVSLYVIRFLTDYVKR
 HDFTIFGKYRIVLGSLLILYWLVVHLF*

Sequence description:

35

A] Length: 579 bp - 193 aa (partial sequence)
 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-68 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-68 gene sequence described in WO 00/06736. N-terminus has yet to be determined.

40

ID-184

Clone 3-11c (ID-121c)

5 ATGGAAATGAAACAAATCAGTCAAACACTGAAAATTACAATTAGTAT
 GGAAGAGTTAGAAGATCGTGGTATGGAGCTGAAAGATTCCTAATCCCTCA
 GGAGAAAGACTGAGGAATTTCTATTCTGTATGGATGAATTAGACTTGCC
 AGAAAACTTAAAAATAGTGGTATGTTAAGTTTCGAGTAACACCTAAAA
 AAGATCGCATTGATGTTTGTACAAAGTCTGAATTAAAGTAAAGATTAA
 ATTAGAAGAATTAGCAGATTGGGTGACATTCAAAAATGTCTCCAGAAG
 ACTTTTAAACCTTGGAACAAATCGATGTTGGAAAAAGGGATACGGAT
 10 GCCCATGCCAAATTAGCAGAAATTGAAAATATGATGGATAAAAGCAACTCA
 AGAAGTAGTTGAGGAAAATGTTCTGAAGAACAAACCTGAAAAGGAAGTAG
 AACGATTGGATATGTTCACTATGTCTTGATTTGATAATTGAAGCTGT
 AGTCGATTTCACAAACGATTGATTCCAATAGAAGCTT
 15 MEMKQISETTLKITISMEDLEDRGMEALKDFLIPQEKTTEFFYSVMDELDLPPENF
 KNSGMLSFRVTPKKDRIDVFVTKSELSKDLNLEELADLGDISKMSPEDFFKTLE
 QSMLEKGDTDAHAKLAEIENMMDKATQEVEENVSEEQPEKEVETIGYVHY
 VFDFDNIEAVVRFSTIDFPIEA

20
 Sequence description:

25 A] Length: 547 bp - 182 aa (Partial sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-68 gene which was identified by LEEP,
 during cloning and sequence analysis of the full-length ID-68 gene sequence.
 ATG start codon is preceded by an typical
 Shine-Dalgarno sequence. No obvious potential
 leader peptide
 30 sequence

35 ID-185
 Clone 3-16b (ID-122b)

40 GGAAACCAACGGCCAGTACAATCGTCAAGGGTAGATTATCCTAAACGTAG
 TCGTGCCAAGATTGAGAAGTTATTTAGACAAGCTCTACTACTGATTA
 TTCTGGTGTTCACAAAGGTTACTATATTGACTTGAAGCCAAGAAACCCG
 GCAGAAAATGCTATGCCTATGAAAAATTTCATGCTCACCAAATAGAGC
 ACATGGCAAATGTATTACAGAAAAAGGGATTGCTTGTCTGCTTCATT

TTTCCACACTTAAGGAAACCTATCTACTCCCTGCTAATGAGTTAATTCAATT
 TTATCAGATTGATAAAGGCAATAAATCAATGCCTATTGATTATATCAGAAA
 AAATGGATTTTCGTAAGGAGAGTGCCTTCCCTCAAGTCCCTACTTAGA
 TATTATTGAAGAAAAATTATTAGGCGGTGATTACAATTAA

5

GNQRPVQSSRVDYPKRSRAKIVEVYFRQASTTDYSGVYKGYYIDFEAKETRQ
 KTAMPMPKNFHAHQIEHMANVLQQKGICFVLLHFSTLKETYLLPANELISFYQI
 DKGNKSMPIDYIRKNGFFVKEAFPQVPYLDIIEKLLGGDYN*

10

Sequence description:

A] Length: 447 bp - 149 aa (partial sequence)

15

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-122 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-122 gene sequence. N-terminus has yet to be determined

20

ID-186

Clone 3-17b (ID-123b)

25

GGATCCTAAAAACGCTAAGGTTATCAAAAAAAATGCTGATCAATTAGTG
 ACAAGGCAATGGCTATTGCAGAGAAGTATAAGCCAAAATTAAAGCTGCA
 AAGTCTAAATACTTTGTGACTTCACATACAGCATTCTCATACTTAGCTAAG
 30 CGATACGGATTGACTCAGTTAGGTATTGCAGGTGTCTCAACCGAGCAAGA
 ACCTAGTGCTAAAAAATTAGCCGAAATTAGGAGTTGTGAAAACATATA
 AGGTTAAGACTATTTTGTGAAGAAGGAGTCTCACCTAAATTAGCTCAAG
 CAGTAGCTTCAGCTACTCGAGTTAAATTGCAAGTTAAGTCCTTAGAAG
 35 CAGTTCCAAAAACAATAAAGATTACTTAGAAAATTGGAAACTAATCTTA
 AGGTACTTGTCAAATCGTTAAATCAATAG

35

DPKNAKVYQKNADQFSDKAMAIKEKYKPKFKAASKYFVTSHTAFSYLAKR
 YGLTQLGIAGVSTEQEPESAKKLAEIQEFVKTYKVKTIFVEEGVSPKLAQAVAS
 40 ATRVKIASLSPLEAVPKNNKDYLENLETNLKVLVKSLNQ*

Sequence description:

A] Length: 433 bp - 144 aa (partial sequence)

5 B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-123 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-123 gene sequence. N-terminus has yet to be determined

10 ID-187

Clone 3-46/47 (ID-130b)

15 ATGAAAAAAAGTCATCGATTAAAAAAACTACAAAAAGCATACGCCTCAGA
AACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAATTGG
ATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTAAA
TGGCATGGAAAAAGCAGATAAGGAAACAGCTCTGTTCTGATACTCAAA
TGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCTCAATCTGATG
20 CCTTACACGAGTCTTAACGGCTTAGAAAATTATTATTCTTGGAAAAAA
TGAAAGGTATTCAAAAAACTGAATTAAAACAGCAGATAACTCATATTCT
AAAGTAGTAGATCTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCA
GAAGGTATGAAAAGACGGCTTCTCTAGCCATGCCCTACTTGGAAACCCC
25 ACAGTTTAATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGG
AGAAAAATCTGGCAAGAGCTAATTAATATTAGGATGAAGGACGTTCTAT
CTTATTACAAACCCACGTTATGGATGAAGCAGAATTAAACAAGTAAGGTTGC
ACTACTATTACGTGGAAACATTATTGCCTTGATACTCCATTACATTAAA
AAAACAATTAAATGTGAGTACTATTGAGGAAGTTCTAAAAGCTGAAGG
30 AGAATAA
35 MKKVIDLKKLQKAYASETVLNNINLEVFKGEIIGLIGPSGAGKSTLIKMLGME
KADKGTALVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLLFFGKMKGIQ
KTELKQQITHISKVVDLENQLDKFVSGYSEGMKRRSLAIALLGNPTVLILDEP
TVGIDPSLRRKIWQELINIKDEGRSIFITTHVMDEAELTSKVALLRGNIIAFDTP
LHLKKQFNVSTIEEVFLKAEGE*

Sequence description:

40 A] Length: 717 bp - 239 aa (Possible full-length sequence)
B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-130 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-130 gene sequence. ATG start codon is preceded by a possible

Shine-Dalgarno. No obvious potential leader peptide sequence

5

ID-188

Clone 3-83b (ID-144b)

10

ATGGTACAAATGATACATGATATGATAAAACAATTGAGCATTGCTGAG
 ACACAAGCTGATTTCCAGTGTATGATATTTAGGGGAAGTCCATACTTAT
 GGACAACCTAAAGTAGACTCTGACTCTAGCTGCTCATATTGATAGCCTA
 GGCCTTGTGAAAAATCACCTGTCTTAGTATTGGTGGTCAAGAATATGAA
 15 ATGTTGGCGACATTGTTGCTTAACAAAGTCAGGGCATGCTTATATACCG
 GTTGACCAACACTCTGCTTGGATAGAATACAGGCTATTATGACAGTTGCT
 CAACCAAGCCTTATCATTCAATTGGTGAATTCCCTCTGAAGTTGATAAT
 GTCCAATCCTAGACGTTCTCAAGTTCAAGCTATTGAGTTGATAAT
 20 CCTTATGAGGTAACACATTCTGTTAAAGGTGATGATAATTACTATATTATT
 TTCACTTCAGGGACTACTGGTTACCAAAAGGTGTGCAAATTTCACATGAC
 AATTATTGAGCTTACAAATTGGATGATTCTGATGATGAGTTTCAGTTC
 CTGAAAGACCGCAAATGTTGGCTCAACCC

25

MVQMIHDMIKTIEHFAETQADFPVYDILGEVHTYQLKVDSDSLAAHIDSLGL
 VEKSPVLVFGGQEYEMLATFVALTKSGHAYIPVDQHSALDRIQAIMTVAQPSL
 IISIGEFPLEVDNVPILDVSQVSAIFEKTPYEVTHSVKGDDNYYIIFTSGTTGLP
 KGVQISHDNLLSFTNWMISDDEFSVPERPQMLAQP

30

Sequence description:

A] Length: 592 bp - 197 aa (partial sequence)

35

B] This gene sequence was not identified using the LEEP system. It was
 identified downstream of the ID-144 gene which was identified by LEEP,
 during cloning and sequence analysis of the full-length ID-144 gene sequence.
 Putative ATG start codon is preceded by a
 typical Shine-Dalgarno sequence. No obvious
 leader peptide sequence

40

This orf is not in frame with nuc

ID-189

Clone 3-86b (ID-145b)

5 ATGGAAAATCATCGTTATGAAGATGAAGGTAATTCCAGCGTAAGATGAC
 CAGTCGTCACTCTTTATGTTATCGCTAGGTGGTATCGGGACTGGGCTT
 TTCTTGAGTTCAAGGTTAACCATTCGACAGGCTGGTCCGTTGGAGCTGTG
 CTGTCTTATTGATTGGTGCCGTTGTGGTTATTGGTCATGCTATCACTTG
 10 GGGAAATTGGCGGTTGCCATGCCGGTGACGGGGTCATTCCACACTTATGCCA
 CTAAGTTATCAGTCCTGGAACAGGTTTACTGTTGCTGGCTATTGGAT
 TTGTTGGACGGTCGCCTGGGGACTGAATTTAGGTGCTGCCATGCTGAT
 GCAGCGCTGGTCCCAAATGTGCCGGCTGGCATTGCTCCTTTTGCC
 15 CTTGTGATTTGGTTAAATGCTTAGCGTAGCCTTTTGCAAGAACAG
 AGTCTTCTCTCAAGTATTAAGGTATTGCTATCATTATCTTATTATCTTG
 GGCTTAGGTGCTATGTTGGCTAGTTCCCTTGAAGGTCAAGCACAAAGGCT
 ATTCTCTCACTCATCTGACTGCCAATGGTGCCTTCAAATGGTATCGTTG
 CAGTTGTCAGTCATGTTGGCTGTTAACTATGCCTCTCTGGTACTGAGTT
 20 AATTGGTATTGCCGGCTGGTGAACGGATAATCCAAAGAACGCTGTACCAA
 GGGCTATTAAAACGACAATCGGTCGCTGGTTGTTTCTTGTACTGACAA
 TTGTTGCCTAGCTTCGCTATTGCAATGAAAGAGGCAGGCGTATCCACAG
 CACCATTGTTGATGTCTTGACAAGATGGAATCCCTTACGGCGGATA
 TCATGAACCTCGTTATCTTGACAGCCATCCTGCTGCTGGTAACTCAGGTCT
 25 CTACGCATCAAGCCGTATGCTCTGGTCCCTGCCAATGAAGGTATGTTGTC
 AAAATCTGTTGAAAATCAATAAACACGGTGTCCAATGCGTGCTCTTCT
 CTTGTCAATGGCAGGAGCAGTGCCTGCTCTTCAAGTATTACGCTGC
 AGACACAGTTATCTAGCCTGGTTCAATCGCGGGCTTGCTGTTGTC
 GTATGGCTAGCCATTCCAGTCGCACAAATCAATTCCGCAAGGAATTG

30 MENHRYEDEGFQRKMTSRHLFMLSLLGGVIGTGLFLSSGYTIAQAGPLGAVL
 SYLIGAVVVYLVMLSLGELAVAMPVTGSFHTYATKFISPGTGFTVAWLYWIC
 WTVALGTEFLGAAMLMQRWFVNVAWAFASFFALVIFGLNALSVRFFAEAES
 FFSSIKVIAIIIFIILGLGAMFGLVSFEGQHKAILFTHLTANGAFPNGIVAVVSVM
 35 LAVNYAFSGTELIGIAAGETDNPKKEAVPRAIKTTIGRLVVFFVLTIVVLASLLPM
 KEAGVSTAPFVDVFDFKMGIPFTADIMNFVILTAISAGNSGLYASSRMLWSLA
 NEGMLSKSVVKINKHGVPMRALLSMAGAVLSLFSSIYAADTVYLALVSIAGF
 AVVVVVWLAIPVAQINFRKEF

40

Sequence description:

A] Length: 1126 bp - 393 aa (partial gene)

sequence)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-145 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-145 gene sequence.

5 Putative ATG start codon is preceded by a typical Shine-Dalgarno sequence. Possesses a possible leader peptide sequence.

10 ID-190

15 Clone 3-94b

20 TCAGAAAATGCAGAGGCAGCAACGGTTGCCACAAACTGGTTACCAAAGG
AGCTAATGTCATTATCGGACCAGCAACATCGGGTGCAGCTGCATCTTCAAC
TCCAAAAGTAAATGCAGCAGCAGTCCAATGATTGCACCTGCTGCGACAC
AAGACAATTAGTCTATGGTTCTGATGGAAAAACCTTAAATCAGTATTCT
25 TCCGAGCTACTTTGTCGATAATTATCAAGGAAAGCTATTGTCAGTATG
CTACAGACAACCTTAAAGCTAAAAAGTTGTTCTATTTATGATAATTAT
CAGATTACTCAAAGGGGGTAGCAAAATCATTAAAGGAAAGTTAGTGGAA
AAAATTGTTGATAGTATGACATTCTCCGCTGGTGTACTGATTCCAAGCG
TCATTGACTAAGTTGAAAGGGAAAGAATATGATGCTATTGATGCCAGG
30 TTACTATACCGAGACAGGATTAATAGTTAAGCAAGCGCGTGATTAGGTAT
CTCTAAACCGGTTCTGGGCCTGATGGTTTGATAGTCCGAAATTGCA
ATCGGCAACACCTGTAGGAGCTCAAACGTTATTATTGACAGGTTCAC
TACACAAGGATCAACCAAAGCTAAAGCT
35 KAKA

40 Sequence description

A] Length: 637 bp - 231 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-149 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-149 gene sequence. N- and C-termini have yet to be determined

5

ID-191

10

Clone 2-c94b (ID-153b)

15

TTGGGACTTAAAGACCATGCTTAGTCTATCCATTTCATTATCTGGGGGG
 CAAAAGCAACGTGTCGCACTAGCTCGTGCATGATGATTGATCCACAGATT
 ATTGGTTATGATGAGCCAAGTAGCGCTTGTATCCAGAGTTGCGTCAAGAA
 GTAGAAAAACTAATTACAAAATAGAGAAACAGGTATGACACAAATTGT
 AGTAACACATGATCTCAATTGCTGAAAGTATATCTGATACGATTCTCAA
 AATTAAATCCTAAGTAG

20

MGLKDHALVYPFSLSGGQKQRVALARAMMIDPQIIGYDEPTSALDPELRQEV
 EKLILQNRETGMTQIVVTHDLQFAESISDTILKINPK*

25

Sequence description

30

A] Length: 270 bp - 90 aa (partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-153 gene which was identified by LEEP, during cloning and sequence analysis of the ID-153 gene sequence.
 N-terminus has yet to be determined

35

ID-192

40

Clone 2-c1b (ID-155b)

ATGACTAATATCTCAGATGTTCCAAAAGCTATTAGAACACAGGCACAGTAT
 GTTCTCTGGGAATGAGAGTTATGGATCAGTCGGTATTACCGAAAACATAT
 AATTCAAAAGAACCTTATTGAAACCAGATATGATTATTCATGATAGA

AGACAAGAGACAATGCTAAAATCACTCAAGAAATAGAAATGGAGCATTG
A

5 MTNISDVPKAIRTQAQYVLLGMRVMDQSVPKTYNSKEPYLKPDIMYIHDRR
QETMLKITQEIMEH*

10 Sequence description

A] Length: 204 bp - 68 aa (partial sequence)
B] This gene sequence was not identified using the LEEP system. It was
15 identified upstream of the ID-155 gene which was identified by LEEP, during
cloning and sequence analysis of the ID-155 gene sequence.
ATG start codon is preceded by a potential typical Shine-Dalgarno sequence.
Has a
typical leader peptide. N-terminus has yet to be
verified

20

ID-193

25 Clone 2-54altb (ID-172b)

30 AAGCTTGCATGCCTGCAGGTGACTCTAGAGGATCTGGGAATATAAATT
TGGATTTCATGACGATGTAAAGCCAATTATTCTACGGGAAAAGGTCTAAA
TGAGGCTGTTATTCGTGAGTTATCTGCAGCTAAGGGTGAACCTGAGTGGAT
GTTGGACTTTCGTCTAAACCTGGAAACGTTAATAAAATGCCATGCA
GACCTGGGGAGCAGATTATCAGATATTGATTTGATGATATTATTATA
35 TCAAAAAGCATCTGATAAACCTGCGCGTGAATGGGATGATGTTCCAGAAA
AAATCAAAGAAACTTTGAAAGAATTGGGATTCAGAAGCTGAAAGAGCC
TATCTGCAGGAGCATCAGCACAATATGAATCAGAAGTAGTTATCACAAT
ATGAAAGAAGAATATGATAAGCTGGGTATTGTTTACGGATACTGACTCT
40 GCACTTAAAGAGTACCCAGAGCTATTCAAAAAATATTTGCTAAACTTGTG
CCTCCAACAGATAATAAATTAGCTGCTCTGAACCTGCTGTATGGTCAGGT
GGAACATTATTATGTTCCCTAAAGGTGTTAAGGTGGATATTCCACTTCAA
ACTTACTTCCGTATTAATAATGAAAATCTGGACAATTGAACGTACTCTC
ATTATTGTTGATGAGGGAGCAAGTGTCACTATGTTGAAGGTTGTACCGCC
CCAACTTATTCTCAAATAGTTACATGCAGCTATAGTTGAAATTTCGAC
TTGATGGAGCTTATATGCGCTATACGACTATTCAAAATTGGTCCGATAATG
TCTATAATTAGTGACAAAACGTGCTACCGCTAAAAAGATGCAACAGTT
GAGTGGATAGATGGAAATCTAGGAGCTAAAACAACAATGAAATACCCATC

GGTTTACCTTGATGGTGAAGGAGCACGTGGCACGATGTTGTCTATTGCTT
TGCAAACAAAGGACAACACCAAGATACTGGGTGCAAAGATGATTCTAAATG
CCCCCCCATACTAGTCATCCATTGTCTCTAAATCAATTGCTAAGGGTGGGG
GAAAAGTTGATTATCGAGGTCAAGTGACATTTAATAAGATTCCAAAAAA
5 TCAGTGTACATATAAGATGTGACACCATAATTGATGGATGATATTCAAAA
TCAGATACCATACCGTTAATGAGATTCTATAATTCACAGGTTGCTTAGAG
CATGAAGCAAAGGTGTCTAAGATTCTGAAGAGCAACTGTACTACTGATG
AGTCGAGGTTATCTGAAGCTGAAGCAACAGAAATGATTGTTATGGGGTTT
GTTGAGCCCTTACGAAAGAATTACCAATGGAATA TGCAGGTTAGAGTTAAA
10 TCGTTAATTCTATGAAATGGAAGGTTAGTTGGTTAA

15 MHACRSTLEDLGEYKFGFHDDVKPIYSTGKGLNEAVIRELSAAKGEPEWMLD
FRLKSLETFNKMPMQTWGADLSIDFDDIIYQKASDKPARDWDDVPEKIKE
TFERIGIPEAERAYLAGASAQYESEVVYHNMKEEYDKLGIVFTDTSALKEYP
ELFKKYFAKLVPPTDNKLAALNSAVWSGGTFIYVPKGVKVDIPLQTYFRINNE
NTGQFERTLIIVDEGASVHYVEGCTAPTYSSNSLHAAIVEIFALDGAYMRYTTI
QNWSNDNVYNLVTKRATAKKDATVEWIDGNLGAKTMMKYPSVYLDGEGARG
TMLSIAFANKGQHQDTGAKMIHNAPHTSSSIVSKSIAKGGGKVDYRGQVTFN
20 KDSKKSVSHIECDTILMDDISKSDTIPFNEIHNSQVALEHEAKVSKISEEQLYYL
MSRGLSEAEATEMIVMGFVEPFTKELPMEYAVELNRLISYEMEGSVG*

Sequence description:

25 A] Length: 1411 bp - 469 aa (Possible full-length gene)
B] This gene sequence was not identified using the LEEP system. It was
identified downstream of the ID-72 gene which was identified by LEEP,
during cloning and sequence analysis of the full-length ID-72 gene sequence.
30 No obvious Shine Dalgarno sequence upstream of
TTG start codon insufficient sequence data). N
terminus needs verification.

35
[D-194]

Clone 3-1b (ID-81b)

40 ATGATAGAATTCTTTCTAATATCAGAACAGAGATCCGCAGATGCCTTA
CTTATCCATAGTTGATTTATCTGTCTTACCTTCTGATGTGGCTGACTTT
GGTTAATAGAGATAAGCCTTGTATAAAACTATTTGGAGTATCCTTTAGG
ACTTCAGTTAATTACGATTATACTTGGTTTCTGGGCAAAATTGCCTTA

TCTGAAAGTCTTCCCCTTACCATTGTCGAATAGGCATGTTGTCGGTCTCTA

5 MIEFFSNIRTEIPQMPLLHSLSLVLPMWLTLVNRDKPLYKTIWSILLGLQLITIYTWF

Sequence description

A) Length: 261 bp - 87 aa (partial gene sequence)

10 B) This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-81 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-81 gene sequence. Sequence Characteristics: Possesses a potential leader peptide sequenceOrf is preceded by a potential Shine-Dalgarno sequence.

15

ID-195

20

Clone RS-55b

25

AAGCTTGTCAAAGTATTAAAGAGATAGGATTAGCTAATGCCATTATTAGCTGTTGCTCCGACAGGGTCAATCAGTTATCTTCTTGTACTCCGAGCC TTCAACCGGTTGTATCACCTGTCGAAGTACGCAAGGAAGGAGCACTGGGG AGGGTTTATGTAGCTGCTTATAAGATTGATGCAGATAATTATGTCTACTAC AAAAAAAGGAGCTTATGAAGTGGGATCTGAGGCGATTATCAATATTGCAGC TGCCGCTCAAAAACACATTGATCAAGCTATTCGTTAACGCTTTCATGAC 30 AGATCAAGCAACTACCGCGAGATTAAATAAAGCCTATATTCAAGCATTAA AACAAAAAATGTGCCTCTATTATTATGTACGAGTGAGACAGGACATCCTAG AAGGTAGCGAGAGTTATGATGATATGCTGGATGATTCACTTCATCGGACT TAGAAGACTGTCAATCCTGCATGATTAA

35

>KLVQSIKEIGLANAHLLAVAPTGSISYLSCTPSLQPVVPVEVRKEGALGRV YVAAYKIDADNYVYYKKGAYEVGSEAIINIAAAAQKHIDQAISLTFMTDQAT TRDLNKAYIQAFKQKCASIYYVRVRQDILEGSESYDDMLDDFTSSDLEDCQSC MI*

40

Sequence description:

A] Length 486 bp - 162 aa (Partial sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-87 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-87 gene sequence. N-terminus to be determined.

5

10 ID-196

Clone RS-59(ID-90b)

15 GTGAGGACATATATTACAAACTTGAATGGACATTCAATCACTAGTACAGC
 ACAAAATAGCTAAAACATGGTAACAGATATAGCAGTAAGCTTAGGTTTC
 GTGAGCTGGGAATACATTCTATCCGATTGATACTGATTCTCCTGAGGAAA
 TGAGTAAGCGTTAGATGGAATCTGTCCGGACTTAGAAAAAAATGATATTG
 TCATATTTCAGACACCTACATGGAACACTACAACACTTTGATGAAAAAATTAT
 20 TTCACAAATTAAAAATATTGGTGTAAAGATTGTTATTTTATACATGATGT
 TGTACCGCTAATGTTGATGGAATTTTATTGATGGATAGAACTATAGC
 TTATTATAATGAAGCAGATGTTAATAGCCCCTAGTCAGCAATGGTCGAT
 AAGCTT

25 MRTYITNLNGHSITSTAQIAQNMVTDIAVSLGFRELGIHSYPIDTDSPEEMSKRL
 DGICSGLRKNDIVFQTPTWNTTFDEKLFLHKLKIFGVKIVIFIHDVVPLMFDGN
 FYLMDRTIAYYNEADVLIAPSQAMVDKL

20

30 Sequence description:

30

A] Length: 414 bp - 138 aa(partial gene)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-90 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-90 gene sequence.

35

No obvious signal peptide, but a

possible Shine Dalgarno sequence is present
 upstream of ATG start codon. C-terminus has yet
 to be determined.

40

ID-197

Clone RS-59c (ID-90c)

5 CATGGAAATGAAGTTGATGATGTTATTAGAAGGGCATTGAATATAATCAC
 CTTATCTTGCTTTGATAATACCTGTCTAACAGAGAGTTAGTATTAGATA
 GCAATATCATTCTCACACAACCTGTGAACAATTGATAAATTAAATGAAAAA
 ATTTATCAGGCTCCATTATGTATTGCTAGAGCAACAAAGAGAACAAACA
 AGTAATGAAACAAAAGAGCGTTATAAAGAAATATTAGGAGGGTATGGAA
 ATGCCTAA

10 HGNEVDDVIRRAFEYNHLIFAFDNTCHNRELVLDNSNIISHTCEQLINLMKNLS
 GSIMYLLQQREQTSNETKERYKEILGGYGNA*

15 Sequence description:

20 A] Length: 261 bp - 87 aa(partial gene sequence)
 B] This gene sequence was not identified using the LEEP system. It was
 identified upstream of the ID-90 gene which was identified by LEEP, during
 cloning and sequence analysis of the full-length ID-90 gene sequence. N-
 terminus has yet to be determined

25 ID-198

Clone RS-70b (ID-93b)

30 ACATTTTATATTATGTATTGAAGACGTAGCCACCCAGTCAAATATGACT
 GGGAAAGATTTTAGTATGTCTAAAGAAGAGTTGTCTATTACCCGTATT
 AAACTTTTAAGAATCAAGGTGTATACAACGGCTTGGTCTATTCTC
 CTTTATGGTTATATATTACAGAATCAAGAAATTGTAGCTATTTTAA
 TCAATGTGTTGCTAGTTGCTTTATGGTGTGTTGACAGTTGATAAAAAAA
 35 TCTTATTAAAACAGGGTGGTTACCTATATTAGCTTTAACATTCTATT
 TTAA

40 TFLYYVFEDVATQSNMTGKIFSMSKEELSYLPVIKLFKNQGVYNGLIGLFLY
 GLYISQNQEIVAIFLINVLLAVYGALTVDKKILLQGGPILALLTFLF*

Sequence description:

A] Length: 312 bp - 104 aa (partial gene sequence)

B] This gene sequence was not identified using the LEEP system. It was identified upstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence.

5 N-terminus has yet to be determined

ID-199

10 Clone RS-70c (ID-93c)

ATGAAATTAAGTGCCTGATTATGGGCTTATTGATTATGGAAAAACTGCA
 AGTGATGCAATACAAGAAACGATTCTTTATCACAAGAGGCGGAGCAACT
 15 AGGCTATCATCAATTGGGTGGCTAACATCACGGTGTAAAGGCATTCAAG
 TATTAGCAATCCAGAATTAATGATAATGCATTGGCTAACAGACTAAATC
 TATCAAAATTGGCTCTGGAGGTATAATGCCTCTGCACTATAGTAGTTAA
 ACTCGCGGAGACTCTCAAGACATTAGAGACATGTCACTCCGAATCGAGTAA
 GTATTGGTTAGGAAATTCACTAGGGACAGTTAAAGTTCAAATGCACTTC
 20 GTAGCTTACATAAAGCACATGATTACGAAGAGGTACTGGAGGAATTGAAG
 TCATGGCTTATTGATGAATCATCCAGTAAGGAACCATTAGTTCAACCGACT
 CTTCTAGCTTCCCAGACTTATATGTGTTGGGAGTGGTCAAAATCAGCT
 TATTAGCGGCTAAACTGGCTTAGGCTTACCTCGGTGTTTCCTTTA
 TGGACAAAGACCCATTGACAGAAGCTAAA

25 MKLSVLDYGLIDYGKTASDAIQETILLSQEAEQLGYHQFWVAEHHGVKA
 FSI
 NPELMIMHLANQTKSIKIGSGGIMPLHYSSFKLAETLKTLETCHPNRVSIGLGN
 SLGTVKVSNALRSLHKAHDYEEVLEELKSWLIDESSSKEPLVQPTLSSFP
 DLYV
 LGSGQKSAYLAALKLGLGFTFGVFPFMDKDPLTEAK

30
 Sequence description:

A] Length: 588 bp - 196 aa (partial)

B] This gene sequence was not identified using the LEEP system. It was identified downstream of the ID-93 gene which was identified by LEEP, during cloning and sequence analysis of the full-length ID-93 gene sequence. No obvious signal peptide, but Shine Dalgarno sequence upstream of the ATG start codon.